GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:34 ; Search time 56.5135 Seconds
(without alignments)
614.956 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLLMGTFLSVSQT.....PVQPEDDADYYCSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	100.0	123	2	AAW75123	Aaw75123 Human sec
2	657	100.0	123	3	AAY66655	Aay66655 Membrane-
3	657	100.0	123	3	AAB24061	Aab24061 Human PRO
4	657	100.0	123	4	AAU12372	Aau12372 Human PRO
5	657	100.0	123	4	AAB65178	Aab65178 Human PRO
6	657	100.0	123	6	ABU57993	Abu57993 Human PRO
7	657	100.0	123	6	ABU59071	Abu59071 Novel hum
8	657	100.0	123	6	ABU82583	Abu82583 Human sec
9	657	100.0	123	6	ABO17816	Abo17816 Novel hum
10	657	100.0	123	6	ABU60502	Abu60502 Human sec
11	657	100.0	123	6	ABU13884	Abu13884 Human PRO
12	657	100.0	123	6	ABU81070	Abu81070 Human PRO
13	657	100.0	123	6	ABU72469	Abu72469 Novel hum
14	657	100.0	123	6	ABU66770	Abu66770 Human PRO
15	657	100.0	123	6	ABU59851	Abu59851 Novel sec
16	657	100.0	123	6	ABU59218	Abu59218 Human sec
17	657	100.0	123	6	ABO25915	Abo25915 Human PRO
18	657	100.0	123	6	ABO25041	Abo25041 Human sec
19	657	100.0	123	6	ABO01999	Abo01999 Novel hum
20	657	100.0	123	6	ABU58924	Abu58924 Human sec
21	657	100.0	123	6	ABU92302	Abu92302 Novel hum
22	657	100.0	123	6	ABU59367	Abu59367 Novel hum
23	657	100.0	123	6	ABU67046	Abu67046 Human sec
24	657	100.0	123	6	ABU92133	Abu92133 Novel hum
25	657	100.0	123	6	ABU10839	Abu10839 Human PRO
26	657	100.0	123	6	ABU81591	Abu81591 Novel hum
27	657	100.0	123	6	ABU88530	Abu88530 Human sec
28	657	100.0	123	6	ABO34044	Abo34044 Human PRO
29	657	100.0	123	6	ADA45921	Ada45921 Novel hum
30	657	100.0	123	6	ADA76352	Ada76352 Human PRO
31	657	100.0	123	6	ADA19002	Ada19002 Human PRO
32	657	100.0	123	6	ADA61625	Ada61625 Homo sapi
33	657	100.0	123	6	ADB19410	Adb19410 Novel hum
34	657	100.0	123	6	ADB27951	Adb27951 Human PRO
35	657	100.0	123	6	ADA86430	Ada86430 Novel hum
36	657	100.0	123	6	ADB15994	Adb15994 Human PRO
37	657	100.0	123	6	ADA37628	Ada37628 Human sec
38	657	100.0	123	6	ADA47780	Ada47780 Human PRO
39	657	100.0	123	6	ADA21314	Ada21314 Human sec
40	657	100.0	123	6	ADA10101	Ada10101 Human sec
41	657	100.0	123	6	ADA67575	Ada67575 Human PRO
42	657	100.0	123	6	ADB30582	Adb30582 Human PRO
43	657	100.0	123	6	ADA85878	Ada85878 Novel hum
44	657	100.0	123	6	ADA17645	Ada17645 Human PRO
45	657	100.0	123	6	ADA97090	Ada97090 Human PRO

ALIGNMENTS

RESULT 1
AAW75123
ID AAW75123 standard; protein; 123 AA.
XX
AC AAW75123;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 67 clone HRGDF73.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US004482.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
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PR 11-APR-1997; 97US-0043670P.

PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
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PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
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PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
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PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
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PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
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PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.

XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 1998-609887/51.
DR N-PSDB; AAV34220.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 320-321; 447pp; English.
XX
CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34145) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC acid sequences AAW75057-W75179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
Db 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy 121 FSP 123
Db 121 FSP 123

RESULT 2
AAY66655
ID AAY66655 standard; protein; 123 AA.
XX
AC AAY66655;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO619.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
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PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
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PR 10-JUN-1998; 98US-0088734P.
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PR 22-JUN-1998; 98US-0090254P.
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PR 26-JUN-1998; 98US-0090863P.
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PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 17-AUG-1998; 98US-0096757P.
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PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
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PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
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PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AAZ64983.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX

PS Claim 12; Fig 68; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
Db 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy 121 FSP 123
Db 121 FSP 123

RESULT 3
AAB24061
ID AAB24061 standard; protein; 123 AA.
XX
AC AAB24061;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO619 protein sequence SEQ ID NO:16.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumourigenesis; identification; cancer; cytostatic;
KW nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000376.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2000-572270/53.
DR N-PSDB; AAC58371.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.
XX
PS Claim 61; Fig 10; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to one of
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC and prevention of cancer. The antibodies and other anti-tumour compounds
CC maybe used to treat various conditions, including those characterised by
CC overexpression and/or activation of the amplified PRO genes. Exemplary
CC conditions or disorders to be treated with such antibodies and other
CC compounds include benign or malignant tumours (e.g., renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC glioblastomas, and various head and neck tumours), leukaemias and
CC lymphoid malignancies, other disorders such as neuronal, glial,
CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC stromal and blastocoelic disorders, and inflammatory, angiogenic and
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC hybridisation probes used in the isolation of the human PRO sequences.
CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
Db 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy 121 FSP 123
Db 121 FSP 123

RESULT 4
AAU12372
ID AAU12372 standard; protein; 123 AA.
XX
AC AAU12372;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO619 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.

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XX
PD   07-JUN-2001.
XX
PF   01-DEC-2000; 2000WO-US032678.
XX
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   09-DEC-1999;   99US-0170262P.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005841.
PR   03-MAR-2000; 2000US-0187202P.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   21-MAR-2000; 2000WO-US007532.
PR   30-MAR-2000; 2000WO-US008439.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   05-JUN-2000; 2000US-0209832P.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI   Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI   Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR   WPI; 2001-408281/43.
DR   N-PSDB; AAS21444.
XX
PT   Isolated , secretory and transmembrane PRO polypeptide used to detect
PT   other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT   polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT   breast, prostate, cervical.
XX
PS   Claim 12; Fig 402; 813pp; English.
XX
CC   AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC   polypeptides. The PRO polypeptides are useful to detect other PRO
CC   polypeptides, to link bioactive molecules to cells expressing PRO
CC   polypeptides, to modulate biological activities of cells expressing PRO
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 657;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-62;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123


RESULT 5
AAB65178
ID   AAB65178 standard; protein; 123 AA.
XX
AC   AAB65178;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW   cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US008439.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   07-JUL-1999;   99US-0143048P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149396P.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   08-OCT-1999;   99US-0158663P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
```

PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44129.
XX
PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 68; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 4; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123
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RESULT 6
ABU57993
ID ABU57993 standard; protein; 123 AA.
XX
AC ABU57993;
XX
DT 14-APR-2003 (first entry)
XX
DE Human PRO polypeptide #25.
XX
KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027163-A1.
XX
PD 06-FEB-2003.
XX
PF 15-NOV-2001; 2001US-00997666.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
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PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
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PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
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PR 24-JUN-1998; 98US-0090540P.
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PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
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PR 25-JUN-1998; 98US-0090694P.
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PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091360P.
PR 01-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091519P.
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PR 02-JUL-1998; 98US-0091633P.
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PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
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PR 04-AUG-1998; 98US-0095318P.
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PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097952P.
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PR 26-AUG-1998; 98US-0097971P.
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PR 26-AUG-1998; 98US-0097978P.
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PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 100.0%; Score 657; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 7
ABU59071
ID ABU59071 standard; protein; 123 AA.
XX
AC ABU59071;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO619.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;

KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
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PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
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PR 04-JUN-1998; 98US-0088028P.
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PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
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PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
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PR 11-FEB-2000; 2000WO-US003565.
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PR 02-MAR-2000; 2000WO-US005841.
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PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-247083/24.
DR N-PSDB; ABX80196.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments.
XX
PS Claim 12; Fig 68; 648pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other

```
CC   nephropathies associated with dermatitis, herpetiformis or Crohn's
CC   disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC   proliferation and/or redifferentiation of chondrocytes in culture and are
CC   thus useful for treating sports injuries, and arthritis. This is the
CC   amino acid sequence of a novel human PRO protein
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 657;  DB 6;  Length 123;
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Qy        121 FSP 123
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Db        121 FSP 123


RESULT 8
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ID   ABU82583 standard; protein; 123 AA.
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AC   ABU82583;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Human secreted/transmembrane protein PRO619.
XX
KW   Human; PRO; secreted protein; transmembrane protein;
KW   cardiac insufficiency disorders; angiogenesis; wound healing;
KW   cancerous tumour; immune response; retinal disorder; sight loss;
KW   retinitis pigmentosum; age-related macular degeneration; AMD;
KW   kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW   Crohn's disease; sports injury; arthritis.
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OS   Homo sapiens.
XX
PN   US2003032023-A1.
XX
PD   13-FEB-2003.
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PF   14-NOV-2001; 2001US-00990711.
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PR 06-JAN-2000; 2000WO-US000376.
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PR 10-MAR-2000; 2000WO-US006319.
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RESULT 9
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AC ABO17816;
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DT 26-AUG-2003 (first entry)
XX
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XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
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PR 31-MAR-1997; 97WO-US005230.
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XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24053.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 402; 660pp; English.
XX
CC The invention describes an isolated nucleic acid (I) comprising, or which
CC has 80 % sequence identity to, or the full-length coding sequence of, one
CC of 275 nucleotide sequences, and which encodes a corresponding
CC polypeptide selected from 275 amino acid sequences, where all sequences
CC are given in the specification. The polypeptide encoded by (I) is used to
CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC the proliferation or differentiation of cells or gene expression,
CC stimulate the release of proteoglycans, stimulate the release of cytokine
CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC acid and polypeptide encoded by it, are useful for treating inflammatory
CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC birth defects, premature aging, acquired immunodeficiency syndrome
CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC hybridisation probes, in chromosome and gene mapping, and in generating
CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123
```

RESULT 10
ABU60502
ID ABU60502 standard; protein; 123 AA.
XX
AC ABU60502;
XX

DT 01-MAY-2003 (first entry)
XX
DE Human secreted/transmembrane protein, #43.
XX
KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW diagnostic; therapeutic; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002160384-A1.
XX
PD 31-OCT-2002.
XX
PF 14-NOV-2001; 2001US-00992598.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
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PR 10-JUN-1998; 98US-0088738P.
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PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
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PR 17-JUN-1998; 98US-0089532P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PSDB; ABX90174.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 68; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 123 AA;

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  Query Match             100.0%;  Score 657;  DB 6;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-62;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123


RESULT 11
ABU13884
ID   ABU13884 standard; protein; 123 AA.
XX
AC   ABU13884;
XX
DT   26-FEB-2003  (first entry)
XX
DE   Human PRO619 polypeptide.
XX
KW   Human; PRO polypeptide; secreted protein; transmembrane protein;
KW   genetic disorder; antibacterial; immunosuppressive.
XX
OS   Homo sapiens.
XX
PN   US2002103125-A1.
XX
PD   01-AUG-2002.
XX
PF   20-NOV-2001; 2001US-00989731.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088025P.
PR   04-JUN-1998;   98US-0088026P.
PR   04-JUN-1998;   98US-0088028P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088738P.
PR   10-JUN-1998;   98US-0088742P.
PR   10-JUN-1998;   98US-0088810P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088826P.
PR   11-JUN-1998;   98US-0088858P.
PR   11-JUN-1998;   98US-0088861P.
PR   11-JUN-1998;   98US-0088876P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089440P.
PR   16-JUN-1998;   98US-0089512P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089532P.
PR   17-JUN-1998;   98US-0089538P.
PR   17-JUN-1998;   98US-0089598P.
PR   17-JUN-1998;   98US-0089599P.
PR   17-JUN-1998;   98US-0089600P.
PR   17-JUN-1998;   98US-0089653P.
PR   18-JUN-1998;   98US-0089801P.
PR   18-JUN-1998;   98US-0089907P.
PR   18-JUN-1998;   98US-0089908P.
PR   16-SEP-1998;   98WO-US019330.
PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   02-JUN-1999;   99WO-US012252.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   06-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   28-AUG-2001; 2001US-00941992.
XX
PA   (GETH ) GENENTECH LTD.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-102117/09.
DR   N-PSDB; ABX64020.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
```

```
XX
PS   Claim 12; Fig 68; 649pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for linking
CC   bioactive molecules to cells expressing PRO polypeptides, for modulating
CC   biological activities of cells expressing PRO polypeptides, and for for
CC   identifying agonists or antagonists. The polynucleotide sequences
CC   encoding PRO polypeptides are useful as hybridisation probes, in
CC   chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC   in the preparation of PRO polypeptides, for generating transgenic animals
CC   or knockout animals, to construct hybridisation probes for mapping the
CC   gene which encodes the PRO polypeptide, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, for chromosome
CC   identification, as chromosome markers, and for generating probes for PCR,
CC   Northern analysis, Southern analysis and Western analysis. ABU13860-
CC   ABU14006 represent the human PRO polypeptides of the invention. Note: The
CC   sequence data for this patent was obtained in electronic format directly
CC   from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 657;  DB 6;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-62;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123.
              |||
Db        121 FSP 123


RESULT 12
ABU81070
ID   ABU81070 standard; protein; 123 AA.
XX
AC   ABU81070;
XX
DT   23-JUN-2003  (first entry)
XX
DE   Human PRO polypeptide #201.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS   Homo sapiens.
XX
PN   US2003004311-A1.
XX
PD   02-JAN-2003.
XX
PF   19-DEC-2001; 2001US-00028072.
XX
PR   18-JUN-1997;   97US-0049911P.
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PR   31-MAR-1998;   98US-0080165P.
PR   12-JUN-1998;   98WO-US012456.
PR   14-JUL-1998;   98WO-US014552.
PR   28-AUG-1998;   98WO-US017888.
PR   10-SEP-1998;   98WO-US018824.
PR   14-SEP-1998;   98WO-US019093.
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PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   29-OCT-1998;   98WO-US022991.
PR   29-OCT-1998;   98WO-US022992.
PR   20-NOV-1998;   98WO-US024855.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
PR   10-MAR-1999;   99WO-US005190.
PR   20-APR-1999;   99WO-US008615.
PR   14-MAY-1999;   99WO-US010733.
PR   02-JUN-1999;   99WO-US012252.
PR   01-SEP-1999;   99WO-US020111.
PR   08-SEP-1999;   99WO-US020594.
PR   13-SEP-1999;   99WO-US020944.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   05-OCT-1999;   99WO-US023089.
PR   29-NOV-1999;   99WO-US028214.
PR   30-NOV-1999;   99WO-US028313.
PR   30-NOV-1999;   99WO-US028409.
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PR   01-DEC-1999;   99WO-US028301.
PR   01-DEC-1999;   99WO-US028634.
PR   02-DEC-1999;   99WO-US028551.
PR   02-DEC-1999;   99WO-US028564.
PR   02-DEC-1999;   99WO-US028565.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   20-DEC-1999;   99WO-US030999.
PR   30-DEC-1999;   99WO-US031243.
PR   30-DEC-1999;   99WO-US031274.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000277.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   18-FEB-2000; 2000WO-US004342.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   01-MAR-2000; 2000WO-US005601.
PR   02-MAR-2000; 2000WO-US005746.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Beresini M,  Deforge L,  Desnoyers L,  Filvaroff E,  Gao W;
PI   Gerritsen ME,  Goddard A,  Godowski PJ,  Gurney AL,  Sherwood S;
PI   Smith V,  Stewart TA,  Tumas D,  Watanabe CK,  Wood WI,  Zhang Z;
XX
DR   WPI; 2003-352836/33.
DR   N-PSDB; ACA67194.
XX
PT   New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT   arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT   heart attack.
XX
PS   Claim 12; Fig 402; 643pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides and polynucleotides are useful for preparing a medicament
CC   useful in the treatment of diabetes, bone and/or cartilage disorders
CC   (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC   hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC   (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC   assays for PRO, by detecting its expression in specific cells, tissues or
CC   serum, and for affinity purification of PRO from recombinant cell culture
CC   or natural sources. ABU80870-ABU81144 represent the human PRO
CC   polypeptides of the invention. Note: The sequence data for this patent
CC   was obtained in electronic format directly from the USPTO web site at
CC   seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 657;  DB 6;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-62;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123


RESULT 13
ABU72469
ID   ABU72469 standard; protein; 123 AA.
XX
AC   ABU72469;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO619.
XX
KW   Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW   virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW   PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW   cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW   lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW   drug screening.
XX
OS   Homo sapiens.
XX
PN   US2003003531-A1.
XX
PD   02-JAN-2003.
XX
PF   19-NOV-2001; 2001US-00989734.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
PR   02-JUN-1998;   98US-0087607P.
PR   02-JUN-1998;   98US-0087609P.
PR   02-JUN-1998;   98US-0087759P.
PR   03-JUN-1998;   98US-0087827P.
PR   04-JUN-1998;   98US-0088021P.
PR   04-JUN-1998;   98US-0088025P.
PR   04-JUN-1998;   98US-0088026P.
PR   04-JUN-1998;   98US-0088028P.
PR   04-JUN-1998;   98US-0088029P.
PR   04-JUN-1998;   98US-0088030P.
PR   04-JUN-1998;   98US-0088033P.
PR   04-JUN-1998;   98US-0088326P.
PR   05-JUN-1998;   98US-0088167P.
PR   05-JUN-1998;   98US-0088202P.
PR   05-JUN-1998;   98US-0088212P.
PR   05-JUN-1998;   98US-0088217P.
PR   09-JUN-1998;   98US-0088655P.
PR   10-JUN-1998;   98US-0088734P.
PR   10-JUN-1998;   98US-0088738P.
PR   10-JUN-1998;   98US-0088742P.
PR   10-JUN-1998;   98US-0088810P.
PR   10-JUN-1998;   98US-0088824P.
PR   10-JUN-1998;   98US-0088826P.
PR   11-JUN-1998;   98US-0088858P.
PR   11-JUN-1998;   98US-0088861P.
PR   11-JUN-1998;   98US-0088876P.
PR   12-JUN-1998;   98US-0089105P.
PR   16-JUN-1998;   98US-0089440P.
PR   16-JUN-1998;   98US-0089512P.
PR   16-JUN-1998;   98US-0089514P.
PR   17-JUN-1998;   98US-0089532P.
PR   17-JUN-1998;   98US-0089538P.
PR   17-JUN-1998;   98US-0089598P.
PR   17-JUN-1998;   98US-0089599P.
PR   17-JUN-1998;   98US-0089600P.
PR   17-JUN-1998;   98US-0089653P.
PR   18-JUN-1998;   98US-0089801P.
PR   18-JUN-1998;   98US-0089907P.
PR   18-JUN-1998;   98US-0089908P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR N-PSDB; ACA64242.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 12; Fig 68; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
Db 1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
Db 61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy 121 FSP 123
Db 121 FSP 123

RESULT 14
ABU66770
ID ABU66770 standard; protein; 123 AA.
XX
AC ABU66770;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #201.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX
PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR N-PSDB; ACA03803.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 402; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 15
ABU59851
ID ABU59851 standard; protein; 123 AA.
XX
AC ABU59851;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO619.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;

KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-00140808.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-148238/14.
DR N-PSDB; ABX89341.
XX
PT Two hundred and seventy five nucleic acids encoding PRO polypeptides,
PT useful for treating pericyte-associated tumors, diabetes and various bone
PT and/or cartilage disorders, e.g. arthritis.
XX
PS Claim 12; Fig 402; 659pp; English.
XX
CC The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of

CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpetiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and are
CC thus useful for treating sports injuries, and arthritis. This is the
CC amino acid sequence of a novel human PRO protein
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 657; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 4.3e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123
```

Search completed: June 28, 2004, 08:26:32
Job time : 57.5135 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:35 ; Search time 14.9595 Seconds
(without alignments)
790.908 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLLMGTFLSVSQT.....PVQPEDDADYYCSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	430	65.4	123	2	S35302	B-cell protein 8HS
2	233.5	35.5	142	2	B28344	VpreB protein prec
3	229.5	34.9	142	2	A28344	VpreB protein prec
4	217.5	33.1	120	2	PS0055	Ig lambda chain pr
5	215.5	32.8	139	2	S00258	VpreB protein - hu
6	215.5	32.8	145	2	I57832	VPre-B protein - h
7	213.5	32.5	232	2	S17399	Ig lambda chain pr
8	210.5	32.0	120	2	PS0056	Ig lambda chain pr
9	208.5	31.7	133	2	A28565	Ig lambda chain pr
10	207.5	31.6	243	2	S25755	Ig lambda chain -
11	202	30.7	111	1	L6HUST	Ig lambda chain V-
12	200.5	30.5	118	2	A32529	Ig lambda chain pr
13	199	30.3	112	1	L6HUAR	Ig lambda chain V-
14	197	30.0	117	2	S04525	Ig lambda chain pr
15	196	29.8	136	2	S16848	Ig lambda chain V-
16	193.5	29.5	98	2	S36068	Ig lambda chain -
17	191.5	29.1	99	2	S36058	Ig lambda chain -
18	191.5	29.1	132	2	A55410	Ig light chain V r
19	191	29.1	235	2	S25758	Ig lambda chain -
20	190.5	29.0	216	2	S69130	Ig lambda chain (D
21	189.5	28.8	234	2	A39956	Ig lambda chain pr
22	186.5	28.4	99	2	S36057	Ig lambda chain -
23	186.5	28.4	111	1	L2HUMC	Ig lambda chain V-
24	185	28.2	111	1	L6HULT	Ig lambda chain V-
25	185	28.2	131	1	L6HUEB	Ig lambda chain pr
26	184.5	28.1	111	1	L2HUBO	Ig lambda chain V-
27	184.5	28.1	233	2	S25744	Ig lambda chain -
28	183.5	27.9	130	1	L1HUBL	Ig lambda chain pr
29	182.5	27.8	99	2	S36051	Ig lambda chain -
30	182.5	27.8	99	2	S36053	Ig lambda chain -
31	182.5	27.8	117	2	S23627	Ig lambda chain pr
32	182.5	27.8	233	2	S25752	Ig lambda chain -
33	182.5	27.8	235	2	S25750	Ig lambda chain -
34	181.5	27.6	111	2	S46397	Ig lambda chain V
35	181.5	27.6	112	2	S31515	Ig lambda chain V
36	181.5	27.6	117	2	S04526	Ig lambda chain pr
37	181.5	27.6	118	2	S12627	Ig lambda chain pr
38	181.5	27.6	234	2	S25757	Ig lambda chain -
39	180.5	27.5	107	2	B46516	Ig lambda chain V
40	180.5	27.5	111	1	L1HUNG	Ig lambda chain V-
41	180.5	27.5	112	1	L2HUNG	Ig lambda chain V-
42	180.5	27.5	117	1	LVHU2	Ig lambda chain pr
43	180.5	27.5	132	2	PL0114	Ig lambda chain pr
44	180.5	27.5	132	2	S04937	Ig lambda chain pr
45	180	27.4	108	2	S38498	Ig lambda chain -

ALIGNMENTS

RESULT 1
S35302
B-cell protein 8HS-20 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C;Accession: S35302
R;Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigemoto, K.; Takebe, Y.; Rajewsky, K.; Ta
EMBO J. 12, 1827-1834, 1993
A;Title: A novel gene product associated with mu chains in immature B cells.
A;Reference number: S35302; MUID:93259124; PMID:8491176
A;Accession: S35302
A;Molecule type: DNA
A;Residues: 1-123 <SHI>
A;Cross-references: EMBL:D13208; NID:g286064; PIDN:BAA02495.1; PID:g286065
C;Genetics:
A;Gene: 8HS-20
A;Introns: 18/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: B-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-123/Product: B-cell protein 8HS-20 #status predicted <MAT>

Query Match 65.4%; Score 430; DB 2; Length 123;
Best Local Similarity 66.1%; Pred. No. 2.9e-36;
Matches 82; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

```
Qy          1 MAC-RCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQ 59
              ||| || ||:|||::| | | | || ||||| | ||||:: || | | |||||||
Db          1 MACPGCLPLLLIGTFVAVFQPTLTQPDAFSVFPGQDAHLSCTINSQHATAGDIGVSWYQQ 60

Qy         60 RAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
               : |||| :|||| :||:|:|||||||||||  | |||||:|||||| |||||||:||: :
Db         61 QPGSAP-HLLYYYAEEEHYRPADIPDRFSATVDAAHNACILTISPVLPEDDADYFCSIAH 119

Qy        120 GFSP 123
               | |
Db        120 TFEP 123
```

RESULT 2
B28344
VpreB protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 05-Nov-1999
C;Accession: B28344
R;Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be s
A;Reference number: A91077; MUID:88029315; PMID:3117530
A;Accession: B28344
A;Molecule type: DNA
A;Residues: 1-142 <KUD>

A;Cross-references: GB:X05563; GB:Y00079; NID:g55415; PIDN:CAA29077.1; PID:g55416
A;Note: the authors translated the codon GAG for residue 110 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;20-142/Product: VpreB protein #status predicted <MAT>

Query Match 35.5%; Score 233.5; DB 2; Length 142;
Best Local Similarity 54.7%; Pred. No. 2.2e-16;
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

```
Qy         33 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 92
              |   :||||||  |  |  | : ||||| |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         93 EAHNACVLTISPVQPEDDADYYCSVG 118
                | |   |:|| :||||:| |||:||
Db         93 TARNLGYLSISELQPEDEAVYYCAVG 118
```

RESULT 3
A28344
VpreB protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C;Accession: A28344
R;Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A;Reference number: A91077; MUID:88029315; PMID:3117530
A;Accession: A28344
A;Molecule type: DNA
A;Residues: 1-142 <KUD>
A;Cross-references: GB:X05556; GB:Y00079; NID:g55409; PIDN:CAA29071.1; PID:g55410
A;Note: the authors translated the codon GAG for residue 110 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match 34.9%; Score 229.5; DB 2; Length 142;
Best Local Similarity 53.5%; Pred. No. 5.6e-16;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

```
Qy         33 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 92
              |   :||||||  |  |  | : ||||| |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         93 EAHNACVLTISPVQPEDDADYYCSVG 118
                |   |:|| :||||:| |||:||
Db         93 TTRNLGYLSISELQPEDEAVYYCAVG 118
```

RESULT 4
PS0055
Ig lambda chain precursor V-II region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C;Accession: PS0055
R;Hayzer, D.J.; Jaton, J.C.
Gene 80, 185-191, 1989
A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lamb
A;Reference number: A91614; MUID:90006781; PMID:2507399
A;Accession: PS0055
A;Molecule type: DNA
A;Residues: 1-120 <HAY>
A;Cross-references: GB:M27840; NID:g341760; PIDN:AAA31363.1; PID:g552407
A;Note: the authors translated the codon TTG for residue 97 as Trp
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig lambda chain V-II region #status predicted <MAT>

Query Match 33.1%; Score 217.5; DB 2; Length 120;
Best Local Similarity 41.2%; Pred. No. 7.6e-15;
Matches 49; Conservative 17; Mismatches 44; Indels 9; Gaps 3;

```
Qy          5 CLSFLLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              |   ||: | |     |:|| || |  ::    |  |:|:|||| | |   | : ||||:
Db          3 CTPLLLLLTLLQCTGSLSQPVLTQSPSVSAALGASAKLTCTLSSAHKT---YTIDWYQQQ 59

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
               | |||||:  :|:  : :   :|||| :   |     | |  || :|:|||||   |
Db         60 QGEAPRYLMQLKSDGSYTKGTGVPDRFSGSSSGADR--YLIIPSVQADDEADYYCGADY 116
```

RESULT 5
S00258
VpreB protein - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Nov-1999
C;Accession: S00258
R;Bauer, S.R.; Kudo, A.; Melchers, F.
EMBO J. 7, 111-116, 1988
A;Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in human
A;Reference number: S00258; MUID:88196069; PMID:3258819
A;Accession: S00258
A;Molecule type: DNA
A;Residues: 1-139 <BAU>
A;Cross-references: EMBL:M34927; NID:g340304; PIDN:AAA61292.1; PID:g340305
C;Genetics:
A;Gene: GDB:VPREB1
A;Cross-references: GDB:120493; OMIM:146770
A;Map position: 22q11.2-22q11.2
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 32.8%; Score 215.5; DB 2; Length 139;
Best Local Similarity 47.0%; Pred. No. 1.4e-14;
Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

```
Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              | || |  |:    |   :|:|||   |  |  | | ||||| |  ||:|| | |: |
Db         20 QPVLHQPPAMSSALGTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKS 78

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVG 118
              :  :| ||| :|| | |   |:|| :||||:| ||::|
Db         79 QGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYYCAMG 118
```

RESULT 6
I57832
VPre-B protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I57832
R;Guelpa-Fonlupt, V.; Bossy, D.; Alzari, P.; Fumoux, F.; Fougereau, M.; Schiff, C.
Mol. Immunol. 31, 1099-1108, 1994
A;Title: The human pre-B cell receptor: structural constraints for a tentative model of
A;Reference number: I57832; MUID:95021318; PMID:7935499
A;Accession: I57832
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <RES>
A;Cross-references: GB:S74019; NID:g693810; PIDN:AAB32118.1; PID:g693811
C;Genetics:
A;Gene: Vpre-B
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 32.8%; Score 215.5; DB 2; Length 145;
Best Local Similarity 47.0%; Pred. No. 1.5e-14;
Matches 47; Conservative 13; Mismatches 39; Indels 1; Gaps 1;

```
Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              | || |  |:    |   :|:|||   |  |  | | ||||| |  ||:|| | |: |
Db         20 QPVLHQPPAMSSALGTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKS 78
```

```
Qy          79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVG 118
               :   :| ||| :|| | |   |:|| :||||:| |||::|
Db          79 QGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYYCAMG 118


RESULT 7
S17399
Ig lambda chain precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17399
R;Hayzer, D.J.; Young-Cooper, G.O.; Mage, R.G.; Jaton, J.C.
Eur. J. Immunol. 20, 2707-2712, 1990
A;Title: cDNA clones encoding immunoglobulin lambda chains from rabbit expressing the ph
A;Reference number: S17399; MUID:91099420; PMID:2125274
A;Accession: S17399
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <HAY>
A;Cross-references: EMBL:X57729; NID:g1593; PIDN:CAA40896.1; PID:g1594
A;Note: the authors translated the codon TTA for residue 92 as Trp and AGC for residue 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

  Query Match             32.5%;  Score 213.5;  DB 2;  Length 232;
  Best Local Similarity   41.7%;  Pred. No. 4e-14;
  Matches   48;  Conservative   18;  Mismatches   40;  Indels    9;  Gaps    3;

Qy           9 LLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSA 64
               ||: | |    |:|| || |  ::    |  |:|:|||| | |   | : ||||: | |
Db           2 LLLLTLLQCTGSLSQPVLTQSPSVSAALGASARLTCTLSSAHKT---YTIDWYQQQQGEA 58

Qy          65 PRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
               ||||:: :|:  : :   :||||| :   |     | |  || :|:|||||   |
Db          59 PRYLMHIKSDGSYTKGTGVPDRFSGSSSGADR--YLIIPSVQADDEADYYCGADY 111


RESULT 8
PS0056
Ig lambda chain precursor V-III region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C;Accession: PS0056
R;Hayzer, D.J.; Jaton, J.C.
Gene 80, 185-191, 1989
A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lamb
A;Reference number: A91614; MUID:90006781; PMID:2507399
A;Accession: PS0056
A;Molecule type: DNA
A;Residues: 1-120 <HAY>
A;Cross-references: GB:M27841; NID:g341761; PIDN:AAA31364.1; PID:g552408
A;Note: the authors translated the codon TTG for residue 97 as Trp
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig lambda chain V-III region #status predicted <MAT>

  Query Match             32.0%;  Score 210.5;  DB 2;  Length 120;
  Best Local Similarity   41.9%;  Pred. No. 3.8e-14;
  Matches   49;  Conservative   16;  Mismatches   43;  Indels    9;  Gaps    3;

Qy           5 CLSFLLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
               |   ||: | |    |:|| || |  :    |  |:|:|||| | |   | : ||||:
Db           3 CTPLLLLLTLLQSTGSLSQPVLTQSPSASAALGSSAKLTCTLSSAHKT---YYIEWYQQQ 59

Qy          61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSV 117
               | |||||:  :|:  : :   :||||| :   |     | || || :|:||| | |
Db          60 QGEAPRYLMQLKSDGSYTKGTGVPDRFSGSSSGADR--YLIISSVQADDEADYICGV 114


RESULT 9
A28565
Ig lambda chain precursor V region (pDH7) - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 18-Oct-1996
C;Accession: A28565
R;Hayzer, D.J.; Jaton, J.C.
J. Immunol. 138, 2316-2322, 1987
A;Title: Nucleotide sequence of a cDNA clone encoding a rabbit immunoglobulin-lambda li
A;Reference number: A92813; MUID:87167587; PMID:3104459
A;Accession: A28565
A;Molecule type: mRNA
A;Residues: 1-133 <HAY>
A;Note: the authors translated the codon TTA for residue 51 as Phe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig lambda chain V region pDH7 #status predicted <MAT>

  Query Match             31.7%;  Score 208.5;  DB 2;  Length 133;
  Best Local Similarity   39.5%;  Pred. No. 6.9e-14;
  Matches   47;  Conservative   18;  Mismatches   45;  Indels    9;  Gaps    3;

Qy           5 CLSFLLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
               |   ||: | |    |:|| || |  :    |  |:|:|||   | |:    ::||||:
Db           3 CTPLLLLLTLLQCTGSLSQPVLTQSPSASATLGASAKLTCTLDSAHKTLH---IAWYQQQ 59

Qy          61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
               | || ||:  :|:  : :   :||||| :   |     | || || :|:|||||   |
Db          60 QGEAPWYLMQLKSDGSYEKGTGVPDRFSGSSSGADR--YLIISSVQADDEADYYCGTDY 116


RESULT 10
S25755
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25755
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25755
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-243 <COM>
A;Cross-references: EMBL:X57820; NID:g33739; PIDN:CAA40957.1; PID:g33740
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;158-226/Domain: immunoglobulin homology <IMM>

  Query Match             31.6%;  Score 207.5;  DB 2;  Length 243;
  Best Local Similarity   40.2%;  Pred. No. 1.7e-13;
  Matches   43;  Conservative   21;  Mismatches   42;  Indels    1;  Gaps    1;

Qy          16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
               |:|| || |  :    |  :|:| ||    :: |: : |||| |: |||||||  |:
Db          17 SLSQPVLTQPSSHSASSGASVRLTCMLS-SGFSVGDFWIRWYQQKPGNPPRYLLYYHSDS 75

Qy          76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFS 122
               :  : : :| ||| : | : || :| || :| | :|||||   :  |
Db          76 NKGQGSGVPSRFSGSNDASANAGILRISGLQLEVEADYYCGTWHSNS 122


RESULT 11
L6HUST
Ig lambda chain V-VI region (SUT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01988
R;Solomon, A.; Kyle, R.A.; Frangione, B.
in Amyloidosis, Glenner, G.G., Osserman, E.F., Benditt, E.P., Calkins, E., Cohn, A.S.,
A;Title: Light chain variable region subgroups of monoclonal immunoglobulins in amyloid
```

```
A;Reference number: A01988
A;Accession: A01988
A;Molecule type: protein
A;Residues: 1-111 <SOL>
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-100/Region: complementarity-determining 3
F;101-111/Region: framework 4
F;22-91/Disulfide bonds: #status predicted

  Query Match             30.7%;  Score 202;  DB 1;  Length 111;
  Best Local Similarity   45.3%;  Pred. No. 2.5e-13;
  Matches   43;  Conservative   15;  Mismatches   31;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   :||| |    ||  | | ||||| | ||  :::    ||  ||
Db          3 MLTQPHSVSESPGKTVIISCTRSDG--TIAGYYVQWYQQRPGRAPTTVIF----EDTQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : | : |:  |||| :| ||:|||||
Db         57 SGVPDRFSGSIDRSSNSASLTISGLQTEDEADYYC 91


RESULT 12
A32529
Ig lambda chain precursor V region (clone pDH8) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Jun-1990 #sequence_revision 23-Nov-1991 #text_change 16-Aug-1996
C;Accession: A32529
R;Hayzer, D.J.; Duvoisin, R.M.; Jaton, J.C.
Biochem. J. 245, 691-697, 1987
A;Title: cDNA clones encoding rabbit immunoglobulin lambda chains. Evidence for length v
A;Reference number: A90338; MUID:88024122; PMID:3117050
A;Accession: A32529
A;Molecule type: mRNA
A;Residues: 1-118 <HAY>
A;Cross-references: GB:M25617
A;Note: the authors translated the codon TTG for residue 37 as Phe
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             30.5%;  Score 200.5;  DB 2;  Length 118;
  Best Local Similarity   42.3%;  Pred. No. 3.8e-13;
  Matches   44;  Conservative   14;  Mismatches   41;  Indels    5;  Gaps    2;

Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              |:|| || |  :     |  |:|:|||   | |     | ||| : | |||||:: | :
Db          3 SLSQPVLTQSPSAAAALGASAKLTCTLDSAHKTSL---VEWYQHQKGEAPRYLMWLRKDG 59

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
              : :   :||||| :   |     | || || :|:||||| | |
Db         60 SYTKGTGVPDRFSGSSSGADR--YLIISSVQADDEADYYCGVDY 101


RESULT 13
L6HUAR
Ig lambda chain V-VI region (AR) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
C;Accession: A01987
R;Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.
Biochem. J. 195, 561-572, 1981
A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-cha
A;Reference number: A01987; MUID:82091000; PMID:6797401
A;Contents: amyloid protein AR
A;Accession: A01987
A;Molecule type: protein
A;Residues: 1-112 <SLE>
A;Note: about half of the lambda chain C region is missing from this protein
C;Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
F;22-91/Disulfide bonds: #status predicted

  Query Match             30.3%;  Score 199;  DB 1;  Length 112;
  Best Local Similarity   44.2%;  Pred. No. 5.1e-13;
  Matches   42;  Conservative   18;  Mismatches   29;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   |||  |    :| |  | ||||| |||| ::|    :|: ||
Db          3 MLTQPHSVSESPGKTVTFSCTGSGG--SIADSFVQWYQQRPGSAPTTVIY----DDNQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : |:: |:  |||| :: ||:|||||
Db         57 SGVPDRFSGSIDDSANSASLTISGLKTEDEADYYC 91


RESULT 14
S04525
Ig lambda chain precursor V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04525
R;Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.
Nucleic Acids Res. 17, 3975, 1989
A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup
A;Reference number: S04525; MUID:89282401; PMID:2499871
A;Accession: S04525
A;Molecule type: DNA
A;Residues: 1-117 <ALE>
A;Cross-references: EMBL:X14615; NID:g33397; PIDN:CAA32769.1; PID:g736246
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-110/Domain: immunoglobulin homology <IMM>

  Query Match             30.0%;  Score 197;  DB 2;  Length 117;
  Best Local Similarity   40.3%;  Pred. No. 8.6e-13;
  Matches   50;  Conservative   23;  Mismatches   41;  Indels   10;  Gaps    5;

Qy          1 MACR-CLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQ 59
              | |   |  ||:    | :|:|| |  ::   |||   :||: |    : :| ||||||
Db          1 MTCSPLLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSSS--DMGNYAVSWYQQ 58

Qy         60 RAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
                |:||: |:|    |:: ||: |||||| :|  :  :  | |: : |||:|||||  : :
Db         59 LPGTAPKLLIY----ENNKRPSGIPDRFSGSK--SGTSATLGITGLWPEDEADYYC-LAW 111

Qy        120 GFSP 123
                ||
Db        112 DTSP 115


RESULT 15
S16848
Ig lambda chain V-II region precursor - human
```

```
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S60297; S16848
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
A;Reference number: S60295; MUID:93122853; PMID:1282498
A;Accession: S60297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KU2>
A;Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

  Query Match             29.8%;  Score 196;  DB 2;  Length 136;
  Best Local Similarity   42.3%;  Pred. No. 1.3e-12;
  Matches   47;  Conservative   18;  Mismatches   38;  Indels    8;  Gaps    4;

Qy          6 LSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAP 65
              |: |  ||  | :|: | |  :    |||   :||| :   |   :| |||||   | ||
Db          8 LTLLTQGTG-SWAQSALTQPPSASGSPGQSVTISCTGTSSDVGAYNY-VSWYQHHPGKAP 65

Qy         66 RYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCS 116
              : ::|  ||    ||: :||||| :|  : |   ||:| :| ||:|||||:
Db         66 KLMMYEVSE----RPSGVPDRFSGSK--SGNTASLTVSGLQAEDEADYYCT 110


Search completed: June 28, 2004, 08:29:57
Job time : 15.9595 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:35 ; Search time 11.0811 Seconds
(without alignments)
577.979 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLLMGTFLSVSQT.....PVQPEDDADYYCSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	100.0	123	1	VPR3_HUMAN	Q9uki3 homo sapien
2	233.5	35.5	142	1	VPR2_MOUSE	P13373 mus musculu
3	229.5	34.9	142	1	VPR1_MOUSE	P13372 mus musculu
4	215.5	32.8	145	1	VPRE_HUMAN	P12018 homo sapien
5	202	30.7	111	1	LV6C_HUMAN	P06317 homo sapien
6	199	30.3	112	1	LV6A_HUMAN	P01721 homo sapien
7	186.5	28.4	111	1	LV2F_HUMAN	P01709 homo sapien
8	185.5	28.2	111	1	LV2L_HUMAN	P80422 homo sapien
9	185	28.2	111	1	LV6D_HUMAN	P06318 homo sapien
10	185	28.2	131	1	LV6E_HUMAN	P06319 homo sapien
11	184.5	28.1	111	1	LV2G_HUMAN	P01710 homo sapien
12	183.5	27.9	130	1	LV1G_HUMAN	P06316 homo sapien
13	180.5	27.5	111	1	LV1D_HUMAN	P01702 homo sapien
14	180.5	27.5	112	1	LV2K_HUMAN	P04209 homo sapien
15	180.5	27.5	117	1	LV0A_HUMAN	P04211 homo sapien
16	179	27.2	111	1	LV2I_HUMAN	P01712 homo sapien
17	177.5	27.0	109	1	LV2E_HUMAN	P01708 homo sapien
18	175	26.6	108	1	LV3A_HUMAN	P01714 homo sapien
19	175	26.6	108	1	LV5A_HUMAN	P01719 homo sapien
20	173	26.3	109	1	LV1F_HUMAN	P04208 homo sapien
21	173	26.3	111	1	LV3B_HUMAN	P80748 homo sapien
22	172.5	26.3	110	1	LV2J_HUMAN	P01713 homo sapien
23	168.5	25.6	111	1	LV2B_HUMAN	P01705 homo sapien
24	167	25.4	106	1	LV4D_HUMAN	P01718 homo sapien
25	166	25.3	106	1	LV4B_HUMAN	P01716 homo sapien
26	166	25.3	111	1	LV1C_HUMAN	P01701 homo sapien
27	165	25.1	107	1	LV4C_HUMAN	P01717 homo sapien
28	164.5	25.0	112	1	LV1B_HUMAN	P01700 homo sapien
29	163.5	24.9	111	1	LV2H_HUMAN	P01711 homo sapien
30	163.5	24.9	112	1	LV1H_HUMAN	P06887 homo sapien
31	163	24.8	106	1	LV4A_HUMAN	P01715 homo sapien
32	162.5	24.7	109	1	KV3D_HUMAN	P01622 homo sapien
33	162.5	24.7	111	1	LV2A_HUMAN	P01704 homo sapien
34	162	24.7	109	1	LV1I_HUMAN	P06888 homo sapien
35	161.5	24.6	129	1	KV3L_HUMAN	P18135 homo sapien
36	160.5	24.4	108	1	KV3A_HUMAN	P01619 homo sapien
37	159.5	24.3	111	1	LV2C_HUMAN	P01706 homo sapien
38	158.5	24.1	111	1	LV2D_HUMAN	P01707 homo sapien
39	158	24.0	113	1	LV1_CHICK	P04210 gallus gall
40	157.5	24.0	109	1	KV3B_HUMAN	P01620 homo sapien
41	157.5	24.0	109	1	KV3G_HUMAN	P04206 homo sapien
42	155.5	23.7	129	1	KV3M_HUMAN	P18136 homo sapien
43	153	23.3	112	1	LV6B_HUMAN	P01722 homo sapien
44	151.5	23.1	115	1	KV3I_HUMAN	P04433 homo sapien
45	151	23.0	106	1	LV4E_HUMAN	P06889 homo sapien

ALIGNMENTS

```
RESULT 1
VPR3_HUMAN
ID   VPR3_HUMAN     STANDARD;      PRT;   123 AA.
AC   Q9UKI3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).
GN   VPREB3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20169186; PubMed=10702669;
RA   Rosnet O., Mattei M.-G., Delattre O., Schiff C.;
RT   "VPREB3: cDNA characterization and expression in human and chromosome
RT   mapping in human and mouse.";
RL   Cytogenet. Cell Genet. 87:205-208(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;
RT   "Molecular cloning of N27C7-2 gene.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.
CC   -!- TISSUE SPECIFICITY: Expressed in B cell precursors. Expressed in
CC       fetal liver, bone marrow, spleen and lymph node.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC   ---------------------------------------------------------------------
```

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CC   ----------------------------------------------------------------------
DR   EMBL; AF163825; AAF09451.1; -.
DR   EMBL; AB050772; BAB83034.1; -.
DR   EMBL; BC020666; AAH20666.1; -.
DR   HSSP; P01709; 2MCG.
DR   Genew; HGNC:12710; VPREB3.
DR   MIM; 605017; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    123       PRE-B LYMPHOCYTE PROTEIN 3.
FT   DOMAIN       21    123       IG-LIKE.
FT   DISULFID     40    115       BY SIMILARITY.
SQ   SEQUENCE   123 AA;  13710 MW;  BF09AC5196059E85 CRC64;

  Query Match             100.0%;  Score 657;  DB 1;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-63;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123


RESULT 2
VPR2_MOUSE
ID   VPR2_MOUSE     STANDARD;      PRT;   142 AA.
AC   P13373;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin omega chain precursor (VpreB2 protein).
GN   VPREB2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X DBA/2J;
RX   MEDLINE=88029315; PubMed=3117530;
RA   Kudo A., Melchers F.;
RT   "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT   appears to be selectively expressed in pre-B lymphocytes.";
RL   EMBO J. 6:2267-2272(1987).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X05563; CAA29077.1; -.
DR   PIR; B28344; B28344.
DR   HSSP; P01607; 1REI.
DR   MGD; MGI:98937; Vpreb2.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    142       IMMUNOGLOBULIN OMEGA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
SQ   SEQUENCE   142 AA;  16052 MW;  7EA7128A4E63D920 CRC64;

  Query Match             35.5%;  Score 233.5;  DB 1;  Length 142;
  Best Local Similarity   54.7%;  Pred. No. 4.7e-18;
  Matches   47;  Conservative    9;  Mismatches   29;  Indels    1;  Gaps    1;

Qy         33 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 92
              |   :||||||  |  |  | : ||||| |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         93 EAHNACVLTISPVQPEDDADYYCSVG 118
              | |   |:|| :|||:| |||:||
Db         93 TARNLGYLSISELQPEDEAVYYCAVG 118


RESULT 3
VPR1_MOUSE
ID   VPR1_MOUSE     STANDARD;      PRT;   142 AA.
AC   P13372;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin iota chain precursor (VPreB1 protein).
GN   VPREB1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X DBA/2J;
RX   MEDLINE=88029315; PubMed=3117530;
RA   Kudo A., Melchers F.;
RT   "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT   appears to be selectively expressed in pre-B lymphocytes.";
RL   EMBO J. 6:2267-2272(1987).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X05556; CAA29071.1; -.
DR   EMBL; X05557; CAA29072.1; -.
DR   PIR; A28344; A28344.
DR   HSSP; P01607; 1REI.
DR   MGD; MGI:98936; Vpreb1.
DR   GO; GO:0005886; C:plasma membrane; IPI.
DR   GO; GO:0004872; F:receptor activity; IPI.
DR   GO; GO:0030097; P:hemopoiesis; IMP.
DR   GO; GO:0006955; P:immune response; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    142       IMMUNOGLOBULIN IOTA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
SQ   SEQUENCE   142 AA;  16125 MW;  2E18BF963A0F448C CRC64;

  Query Match             34.9%;  Score 229.5;  DB 1;  Length 142;
  Best Local Similarity   53.5%;  Pred. No. 1.3e-17;
  Matches   46;  Conservative    9;  Mismatches   30;  Indels    1;  Gaps    1;

Qy         33 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 92
              |    :||||||  |   |  | : ||||| |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         93 EAHNACVLTISPVQPEDDADYYCSVG 118
                 |   |:|| :||||:| |||:||
Db         93 TTRNLGYLSISELQPEDEAVYYCAVG 118


RESULT 4
VPRE_HUMAN
ID   VPRE_HUMAN     STANDARD;      PRT;   145 AA.
AC   P12018;
DT   01-OCT-1989 (Rel. 12, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin iota chain precursor (V(pre)B protein) (VpreB protein)
DE   (CD179a antigen).
GN   VPREB1 OR VPREB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021318; PubMed=7935499;
RA   Guelpa-Fonlupt V., Bossy D., Alzari P., Fumoux F., Fougereau M.,
RA   Schiff C.;
RT   "The human pre-B cell receptor: structural constraints for a tentative
RT   model of the pseudo-light (psi L) chain.";
RL   Mol. Immunol. 31:1099-1108(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97228902; PubMed=9074928;
RA   Kawasaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,
RA   Schmeits J.L., Wang J., Shimizu N.;
RT   "One-megabase sequence analysis of the human immunoglobulin lambda
RT   gene locus.";
RL   Genome Res. 7:250-261(1997).
RN   [3]
RP   SEQUENCE OF 1-139 FROM N.A.
RX   MEDLINE=88196069; PubMed=3258819;
RA   Bauer S.R., Kudo A., Melchers F.;
RT   "Structure and pre-B lymphocyte restricted expression of the VpreB in
RT   humans and conservation of its structure in other mammalian
RT   species.";
RL   EMBO J. 7:111-116(1988).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- SUBUNIT: Associates non-covalently with IGLL1.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 1:59-63(2000);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/574153212_g.htm".
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D86992; BAA19987.1; -.
DR   EMBL; D88270; BAA20030.1; -.
DR   EMBL; S74019; AAB32118.1; -.
DR   EMBL; M34927; AAA61292.1; -.
DR   PIR; I57832; I57832.
DR   PIR; S00258; S00258.
DR   HSSP; P80748; 2LOI.
DR   Genew; HGNC:12709; VPREB1.
DR   MIM; 605141; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Antigen; Signal; Immunoglobulin domain.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    145       IMMUNOGLOBULIN IOTA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   CONFLICT     10     10       L -> H (IN REF. 3).
SQ   SEQUENCE   145 AA;  16605 MW;  197665B13AF64D46 CRC64;

  Query Match             32.8%;  Score 215.5;  DB 1;  Length 145;
  Best Local Similarity   47.0%;  Pred. No. 4.1e-16;
  Matches   47;  Conservative   13;  Mismatches   39;  Indels    1;  Gaps    1;

Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              | || |  |:    |   :|:|||   |  | | | |||||  |  ||:|| | |: |
Db         20 QPVLHQPPAMSSALGTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKS 78

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVG 118
              :   :| ||| :|| | |    |:|| :||||:| |||:|
Db         79 QGPQVPPRFSGSKDVARNRGYLSISELQPEDEAMYYCAMG 118


RESULT 5
LV6C_HUMAN
ID   LV6C_HUMAN     STANDARD;      PRT;   111 AA.
AC   P06317;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region SUT.
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RA   Solomon A., Kyle R.A., Frangione B.;
RT   "Light chain variable region subgroups of monoclonal immunoglobulins
RT   in amyloidosis AL.";
RL   (In) Glenner G.G., Osserman E.F., Benditt E.P., Calkins E.,
RL   Cohen A.S., Zucker-Franklin D. (eds.);
RL   Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR   PIR; A01988; L6HUST.
DR   PDB; 1CD0; 06-MAR-00.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   DOMAIN        1     22       FRAMEWORK-1.
FT   DOMAIN       23     35       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       36     50       FRAMEWORK-2.
FT   DOMAIN       51     57       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       58     91       FRAMEWORK-3.
FT   DOMAIN       92    100       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      101    111       FRAMEWORK-4.
FT   DISULFID     22     91       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12247 MW;  0941DD547D983598 CRC64;

  Query Match             30.7%;  Score 202;  DB 1;  Length 111;
  Best Local Similarity   45.3%;  Pred. No. 8.5e-15;
  Matches   43;  Conservative   15;  Mismatches   31;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   :||| |    ||  | | ||||| | ||  :::    ||  ||
Db          3 MLTQPHSVSESPGKTVIISCTRSDG--TIAGYYVQWYQQRPGRAPTTVIF----EDTQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : | : |:  |||| :| ||:|||||
Db         57 SGVPDRFSGSIDRSSNSASLTISGLQTEDEADYYC 91


RESULT 6
LV6A_HUMAN
ID   LV6A_HUMAN     STANDARD;      PRT;   112 AA.
AC   P01721;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region AR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (AMYLOID PROTEIN AR).
RX   MEDLINE=82091000; PubMed=6797401;
RA   Sletten K., Natvig J.B., Husby G., Juul J.;
RT   "The complete amino acid sequence of a prototype
RT   immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";
RL   Biochem. J. 195:561-572(1981).
CC   -!- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING
CC       FROM THIS PROTEIN.
CC   -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A
CC       PATIENT WITH AMYLOIDOSIS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01987; L6HUAR.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1    107       IG-LIKE.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11918 MW;  570BCD9A368EF1FE CRC64;

  Query Match             30.3%;  Score 199;  DB 1;  Length 112;
  Best Local Similarity   44.2%;  Pred. No. 1.8e-14;
  Matches   42;  Conservative   18;  Mismatches   29;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   |||  |    :| |  | |||||  ||||  ::|    :|: ||
Db          3 MLTQPHSVSESPGKTVTFSCTGSGG--SIADSFVQWYQQRPGSAPTTVIY----DDNQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : |:: |:  ||||  :: ||:|||||
Db         57 SGVPDRFSGSIDDSANSASLTISGLKTEDEADYYC 91


RESULT 7
LV2F_HUMAN
ID   LV2F_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01709;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region MGC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [2]
RP   LAMBDA CHAIN GENES.
RX   MEDLINE=76093781; PubMed=812801;
RA   Fett J.W., Deutsch H.F.;
RT   "A new lambda-chain gene.";
RL   Immunochemistry 12:643-652(1975).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC       A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC       SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90381; L2HUMC.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 1A8J; 17-JUN-98.
DR   PDB; 1DCL; 15-MAY-97.
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DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    108       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   STRAND        5      5
FT   STRAND       10     12
FT   STRAND       18     23
FT   TURN         26     32
FT   STRAND       36     40
FT   TURN         42     43
FT   STRAND       50     51
FT   TURN         52     54
FT   STRAND       55     55
FT   TURN         62     63
FT   STRAND       66     68
FT   STRAND       72     77
FT   HELIX        82     84
FT   STRAND       86     93
FT   STRAND       99    101
FT   STRAND      105    109
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11558 MW;  7CC1D6E2FA3377BA CRC64;

  Query Match             28.4%;  Score 186.5;  DB 1;  Length 111;
  Best Local Similarity   43.9%;  Pred. No. 4e-13;
  Matches   43;  Conservative   16;  Mismatches   32;  Indels    7;  Gaps    3;

Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              |: | |  :     ||   :||| :   |   :| |||||| || ||: ::|    | :
Db          1 QSALTQPPSASGSLGQSVTISCTGTSSDVGGYNY-VSWYQQHAGKAPKVIIY----EVNK 55

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCS 116
              ||: :||||| :|  : |   ||:| :| ||:||||||
Db         56 RPSGVPDRFSGSK--SGNTASLTVSGLQAEDEADYYCS 91


RESULT 8
LV2L_HUMAN
ID   LV2L_HUMAN     STANDARD;      PRT;   111 AA.
AC   P80422;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma lambda chain V-II region DOT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    106       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11787 MW;  F358B1EA2CD7109A CRC64;

  Query Match             28.2%;  Score 185.5;  DB 1;  Length 111;
  Best Local Similarity   44.8%;  Pred. No. 5.1e-13;
  Matches   43;  Conservative   14;  Mismatches   32;  Indels    7;  Gaps    3;

Qy         20 TVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHR 79
              : | |  :|   |||  :|||  |  |   |  ||||||  | ||| |:|    :|  |
Db          2 SALTQPRSLSGSPGQAVTISCTGLPS-VVDDDNFVSWYQQTPGRAPRLLIY----DDSLR 56

Qy         80 PADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              |: :|:||| :| :   |  |||| :||:|:| |:|
Db         57 PSGVPNRFSGSKSDTKAA--LTISGLQPDDEATYFC 90


RESULT 9
LV6D_HUMAN
ID   LV6D_HUMAN     STANDARD;      PRT;   111 AA.
AC   P06318;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region WLT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86122667; PubMed=4089539;
RA   Dwulet F.E., Strako K., Benson M.D.;
RT   "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RT   (WLT).";
RL   Scand. J. Immunol. 22:653-660(1985).
DR   PIR; A01989; L6HULT.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     22       FRAMEWORK-1.
FT   DOMAIN       23     35       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       36     50       FRAMEWORK-2.
FT   DOMAIN       51     57       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       58     91       FRAMEWORK-3.
FT   DOMAIN       92    101       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      102    111       FRAMEWORK-4.
FT   DISULFID     22     91       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11966 MW;  0C88B2FE37BCE24F CRC64;

  Query Match             28.2%;  Score 185;  DB 1;  Length 111;
  Best Local Similarity   45.2%;  Pred. No. 5.7e-13;
  Matches   38;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    2;

Qy         32 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 91
              | :   :||| |    :|    | ||||| |||| ::|    |:: ||:::|||| :
Db         14 PEKTVTISCTGSSG--SIGSNYVQWYQQRPGSAPTNVIY----ENNQRPSEVPDRFSGSI 67

Qy         92 DEAHNACVLTISPVQPEDDADYYC 115
              | : |:  |||| :: ||:|||||
Db         68 DSSSNSASLTISGLKTEDEADYYC 91
```

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RESULT 10
LV6E_HUMAN
ID   LV6E_HUMAN     STANDARD;      PRT;   131 AA.
AC   P06319;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region EB4 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85215660; PubMed=3923440;
RA   Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT   "Cloning and sequence analysis of an Ig lambda light chain mRNA
RT   expressed in the Burkitt's lymphoma cell line EB4.";
RL   Nucleic Acids Res. 13:2931-2941(1985).
DR   PIR; A01990; L6HUEB.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    131       IG LAMBDA CHAIN V-VI REGION EB4.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    110       FRAMEWORK-3.
FT   DOMAIN      111    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      119    131       FRAMEWORK-4.
FT   DISULFID     41    110       BY SIMILARITY.
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  14147 MW;  02A9179C8C05C2CD CRC64;

  Query Match             28.2%;  Score 185;  DB 1;  Length 131;
  Best Local Similarity   42.1%;  Pred. No. 6.9e-13;
  Matches   40;  Conservative   16;  Mismatches   33;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :|  |   ::   ||:   :|||      :|     | |||||  |||  ::|    ||: ||
Db         22 MLTQPHSVSESPGKTVTISCT--GNSGSIASNYVQWYQQRRVSAPTIVIY----EDNQRP 75

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
                :|||||  :  |  :  |:  ||||  ::  ||:|||||
Db         76 LGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYC 110


RESULT 11
LV2G_HUMAN
ID   LV2G_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01710;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region BO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71103825; PubMed=5532228;
RA   Wikler M., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT   chymotryptic peptides, and sequence of protein Bo.";
RL   J. Biol. Chem. 245:4488-4507(1970).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01976; L2HUBO.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11785 MW;  92F5A1BF72421BAC CRC64;

  Query Match             28.1%;  Score 184.5;  DB 1;  Length 111;
  Best Local Similarity   41.8%;  Pred. No. 6.5e-13;
  Matches   41;  Conservative   16;  Mismatches   34;  Indels    7;  Gaps    3;

Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              |: | |  :    |||   :||| :   |    | ||||||  | ||: :::    |
Db          1 QSALTQPPSASGSPGQSVTISCTGTSSDVGDNKY-VSWYQQHPGRAPKLVIF----EVSQ 55

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCS 116
              ||: :|||||  :| :  |    ||:| :: ||:||||||
Db         56 RPSGVPDRFSGSKSD--NTASLTVSGLRAEDEADYYCS 91


RESULT 12
LV1G_HUMAN
ID   LV1G_HUMAN     STANDARD;      PRT;   130 AA.
AC   P06316;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-I region BL2 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85062823; PubMed=6095199;
RA   Tsujimoto Y., Croce C.M.;
RT   "Molecular cloning of a human immunoglobulin lambda chain variable
RT   sequence.";
RL   Nucleic Acids Res. 12:8407-8414(1984).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X01147; CAA25598.1; -.
DR   PIR; A01966; L1HUBL.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    130       IG LAMBDA CHAIN V-I REGION BL2.
FT   DOMAIN       20    115       V SEGMENT.
FT   DOMAIN      116    130       J SEGMENT.
FT   DISULFID     41    108       BY SIMILARITY.
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  13564 MW;  FA44BB17D3A55EBF CRC64;

  Query Match             27.9%;  Score 183.5;  DB 1;  Length 130;
  Best Local Similarity   40.5%;  Pred. No. 1e-12;
  Matches   47;  Conservative   22;  Mismatches   38;  Indels    9;  Gaps    5;

Qy          1 MACR-CLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQ 59
              | |  |  ||:   | :|:|| |  ::   |||   :||: |  ::   || ||||||
Db          1 MTCSPLLLTLLIHCTGSWAQSVLTQPPSVSAAPGQKVTISCSGSSSNIG-NDY-VSWYQQ 58

Qy         60 RAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
                |:||: |:|    ::: ||: |||||| :|  :  :  | |: :|  |:|||||
Db         59 VPGTAPKLLIY----DNNKRPSGIPDRFSGSK--SGTSATLGITGLQTGDEADYYC 108


RESULT 13
LV1D_HUMAN
ID   LV1D_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01702;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-I region NIG-64.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83186114; PubMed=6404900;
RA   Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
RA   Shimizu A.;
RT   "Comparative studies on the structure of the light chains of human
RT   immunoglobulins. IV. Assignment of a subsubgroup.";
RL   J. Biochem. 93:421-429(1983).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01965; L1HUNG.
DR   HSSP; P01703; 7FAB.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    105       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     89       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11454 MW;  A21C6121C18A61E0 CRC64;

  Query Match             27.5%;  Score 180.5;  DB 1;  Length 111;
  Best Local Similarity   41.1%;  Pred. No. 1.7e-12;
  Matches   44;  Conservative   19;  Mismatches   29;  Indels   15;  Gaps    4;

Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              |:|| |  ::   |||   :||: |  :  | |  ||||||  |:||: |:|    :::
Db          1 QSVLTQPPSVSAAPGQEVTISCSGSSSN--IGDNFVSWYQQLPGTAPKLLIY----DNNK 54

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC-------SVG 118
              ||: ||||||  :|  :  :  | |: :|  |:|||||       |||
Db         55 RPSGIPDRFSGSK--SGTSATLGITGLQTGDEADYYCGTWDSSLSVG 99


RESULT 14
LV2K_HUMAN
ID   LV2K_HUMAN     STANDARD;      PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC       INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT   DOMAIN        1    102       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11581 MW;  988FEF363AE1E4F3 CRC64;

  Query Match             27.5%;  Score 180.5;  DB 1;  Length 112;
  Best Local Similarity   43.9%;  Pred. No. 1.8e-12;
  Matches   43;  Conservative   16;  Mismatches   32;  Indels    7;  Gaps    3;

Qy         19 QTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              |: | |  ::   |||   :||| :   |   |: ||||||  | ||: |:|    : :
Db          1 QSALTQPASVSGSPGQSITISCTGTTSDVGGYDF-VSWYQQHPGKAPKLLIY----DVNS 55

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCS 116
              ||: | :||| :|  : |   |||| :| ||:||||||
Db         56 RPSGISNRFSGSK--SGNTASLTISGLQAEDEADYYCS 91


RESULT 15
LV0A_HUMAN
ID   LV0A_HUMAN     STANDARD;      PRT;   117 AA.
AC   P04211;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V region 4A precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014122; PubMed=6091030;
RA   Anderson M.L.M., Szajnert M.F., Kaplan J.C., McColl L.,
RA   Young B.D.;
RT   "The isolation of a human Ig V lambda gene from a recombinant library
RT   of chromosome 22 and estimation of its copy number.";
RL   Nucleic Acids Res. 12:6547-6661(1984).
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DR   PIR; A01993; LVHU2.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    117       IG LAMBDA CHAIN V REGION 4A.
FT   DOMAIN       21     42       FRAMEWORK-1.
FT   DOMAIN       43     55       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       56     71       FRAMEWORK-2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       79    110       FRAMEWORK-3.
FT   DOMAIN      111    117       COMPLEMENTARITY-DETERMINING-3.
FT   DISULFID     42    110       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12380 MW;  C587B0047CC1CD62 CRC64;

  Query Match             27.5%;  Score 180.5;  DB 1;  Length 117;
  Best Local Similarity   42.9%;  Pred. No. 1.9e-12;
  Matches   45;  Conservative   13;  Mismatches   40;  Indels    7;  Gaps    3;

Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              | ||||: |  :| | ||    |:|  |   ||   |  :|:||: | ||| |:|  | :
Db         18 SNSQTVVTQEPSLTVSPGGTVTLTCASSTGAVT-SGYYPNWFQQKPGQAPRALIYSTSNK 76

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
                 ||    ||| :          ||:| |||||:|:||| : ||
Db         77 HSWTPA----RFSGSL--LGGKAALTLSGVQPEDEAEYYCLLYYG 115


Search completed: June 28, 2004, 08:29:16
Job time : 11.0811 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:34 ; Search time 40.4459 Seconds
(without alignments)
959.521 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLLMGTFLSVSQT.....PVQPEDDADYYCSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	430	65.4	123	11	Q61243	Q61243 mus musculu
2	235.5	35.8	230	4	Q7Z2U3	Q7z2u3 homo sapien
3	199	30.3	112	4	Q96JD1	Q96jd1 homo sapien
4	199	30.3	135	4	Q9H5Z4	Q9h5z4 homo sapien
5	194	29.5	112	4	Q96JD2	Q96jd2 homo sapien
6	191.5	29.1	116	4	Q96JD0	Q96jd0 homo sapien
7	190.5	29.0	236	4	Q96E61	Q96e61 homo sapien
8	187	28.5	237	4	Q8WTU6	Q8wtu6 homo sapien
9	184.5	28.1	237	4	Q8WUK4	Q8wuk4 homo sapien
10	182	27.7	240	4	Q8WUK3	Q8wuk3 homo sapien
11	178	27.1	234	4	Q8N355	Q8n355 homo sapien
12	174	26.5	235	11	Q99M11	Q99m11 mus musculu
13	171	26.0	107	4	Q9NSD6	Q9nsd6 homo sapien
14	170	25.9	233	4	Q8TBC9	Q8tbc9 homo sapien
15	170	25.9	234	4	Q7Z2U7	Q7z2u7 homo sapien
16	169.5	25.8	236	4	Q8NEJ1	Q8nej1 homo sapien
17	168	25.6	108	4	Q96SB0	Q96sb0 homo sapien
18	167.5	25.5	109	4	Q9UL86	Q9ul86 homo sapien
19	166	25.3	100	6	O77624	O77624 bos taurus
20	166	25.3	110	4	Q8TE63	Q8te63 homo sapien
21	164	25.0	233	4	Q96I69	Q96i69 homo sapien
22	164	25.0	233	4	Q8N5F4	Q8n5f4 homo sapien
23	159.5	24.3	109	4	Q9UL78	Q9ul78 homo sapien
24	158.5	24.1	105	4	Q8WVJ6	Q8wvj6 homo sapien
25	156	23.7	81	4	Q7Z2E8	Q7z2e8 homo sapien
26	154.5	23.5	132	4	Q8TBD0	Q8tbd0 homo sapien
27	154	23.4	107	4	Q9UL82	Q9ul82 homo sapien
28	151	23.0	101	4	Q8IZD8	Q8izd8 homo sapien
29	147	22.4	248	13	Q7SYU1	Q7syu1 xenopus lae
30	145.5	22.1	131	11	Q811C3	Q811c3 mus musculu
31	140.5	21.4	108	4	Q9UL83	Q9ul83 homo sapien
32	136.5	20.8	484	11	Q8VEA0	Q8vea0 mus musculu
33	136	20.7	129	11	Q8VDE2	Q8vde2 mus musculu
34	135.5	20.6	109	4	Q9UL85	Q9ul85 homo sapien
35	135.5	20.6	113	11	Q8CGS1	Q8cgs1 mus musculu
36	134	20.4	97	4	O43234	O43234 homo sapien
37	134	20.4	107	11	Q9ERZ9	Q9erz9 mus musculu
38	134	20.4	235	11	Q91W12	Q91w12 mus musculu
39	134	20.4	237	13	Q7SZ36	Q7sz36 xenopus lae
40	133.5	20.3	93	4	Q9UL76	Q9ul76 homo sapien
41	131.5	20.0	111	11	Q811U6	Q811u6 mus musculu
42	131	19.9	235	11	Q7TMK0	Q7tmk0 mus musculu
43	131	19.9	239	4	Q8NEK0	Q8nek0 homo sapien
44	130.5	19.9	99	11	Q9JL74	Q9jl74 mus musculu
45	130.5	19.9	108	4	Q9UL79	Q9ul79 homo sapien

ALIGNMENTS

RESULT 1
Q61243
ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 8HS20 protein precursor (Pre-B lymphocyte gene 3).
GN VPREB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBO J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; D13208; BAA02495.1; -.
DR   EMBL; AK008794; BAB25899.1; -.
DR   PIR; S35302; S35302.
DR   HSSP; P01709; 2MCG.
DR   MGD; MGI:98938; Vpreb3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   CHAIN        20    123       8HS20 PROTEIN.
SQ   SEQUENCE   123 AA;  13400 MW;  2A1AD371D1CEB98F CRC64;

  Query Match             65.4%;  Score 430;  DB 11;  Length 123;
  Best Local Similarity   66.1%;  Pred. No. 1.2e-40;
  Matches   82;  Conservative   14;  Mismatches   26;  Indels    2;  Gaps    2;

Qy          1 MAC-RCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQ 59
              ||| ||  ||:|||::| |  | | ||  ||||| | ||||:: || |  | |||||||
Db          1 MACPGCLPLLLIGTFVAVFQPTLTQPDAFSVFPGQDAHLSCTINSQHATAGDIGVSWYQQ 60

Qy         60 RAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGY 119
              : |||| :|||| :||:|:|||||||||||  | |||||:|||||| |||||||:||: :
Db         61 QPGSAP-HLLYYYAEEEHYRPADIPDRFSATVDAAHNACILTISPVLPEDDADYFCSIAH 119

Qy        120 GFSP 123
               | |
Db        120 TFEP 123


RESULT 2
Q7Z2U3
ID   Q7Z2U3      PRELIMINARY;      PRT;   230 AA.
AC   Q7Z2U3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054893; AAH54893.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   230 AA;  24853 MW;  8BE60CC824BB886E CRC64;

  Query Match             35.8%;  Score 235.5;  DB 4;  Length 230;
  Best Local Similarity   45.5%;  Pred. No. 2.4e-18;
  Matches   46;  Conservative   21;  Mismatches   33;  Indels    1;  Gaps    1;

Qy         17 VSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEED 76
              :|| || |  :|    ||  | |:|||  :   : || : ||||::| :|:||| :||: |
Db          8 LSQAVLTQPSSLSASPGASASLTCTLR-RGFYVVYDYRIYWYQQKSGRSPQYLLRHRSDSD 66

Qy         77 HHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSV 117
                : : :| ||| :|| : || :| || :: ||:||||| |
Db         67 KQQGSGVPSRFSGSKDASANAGILVISGLRSEDEADYYCMV 107


RESULT 3
Q96JD1
ID   Q96JD1      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region PIP (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region PIP.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267874; AAK58586.1; -.
DR   PIR; A30323; A30323.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12047 MW;  0D3885AC23567B9F CRC64;

  Query Match             30.3%;  Score 199;  DB 4;  Length 112;
  Best Local Similarity   44.2%;  Pred. No. 1.3e-14;
  Matches   42;  Conservative   17;  Mismatches   30;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:  :||| |   :|    | ||||| |||| ::|    ||: ||
Db          3 MLTQPHSVSESPGKTITISCTRSSG--SIASNYVQWYQQRPGSAPTTVIY----EDNQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : | : |:  |||| :: ||:|||||
Db         57 SGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYC 91


RESULT 4
Q9H5Z4
ID   Q9H5Z4      PRELIMINARY;      PRT;   135 AA.
AC   Q9H5Z4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ22755.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ileal mucosa;
RA   Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA   Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA   Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA   Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA   Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK026408; BAB15473.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   135 AA;  14780 MW;  652492DED930F401 CRC64;

  Query Match             30.3%;  Score 199;  DB 4;  Length 135;
  Best Local Similarity   45.3%;  Pred. No. 1.7e-14;
  Matches   34;  Conservative   17;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         48 TIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQP 107
              :: |: : ||||: |: ||||||| |: :  : : :| ||| : | : || :| || :||
Db          7 SVGDFWIRWYQQKPGNPPRYLLYYHSDSNKGQGSGVPSRFSGSNDASANAGILRISGLQP 66

Qy        108 EDDADYYCSVGYGFS 122
              ||:|||||   :  |
Db         67 EDEADYYCGTWHSNS 81


RESULT 5
Q96JD2
ID   Q96JD2      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region NEG (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region NEG.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267873; AAK58585.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     112     112
SQ   SEQUENCE   112 AA;  11908 MW;  080B4B37E2360B06 CRC64;

  Query Match             29.5%;  Score 194;  DB 4;  Length 112;
  Best Local Similarity   43.2%;  Pred. No. 4.9e-14;
  Matches   41;  Conservative   16;  Mismatches   32;  Indels    6;  Gaps    2;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   :||| |     |    | ||||| |||| ::|    |:: ||
Db          3 MLTQPHSVSGSPGKTITISCTGSSGR--IASNSVQWYQQRPGSAPNIVMY----ENNQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              : :||||| : | : |:  |||| :  ||:|||||
Db         57 SGVPDRFSGSIDSSSNSASLTISGLMTEDEADYYC 91


RESULT 6
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Q96JD0
ID   Q96JD0      PRELIMINARY;      PRT;  116 AA.
AC   Q96JD0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region SAR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region SAR.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267875; AAK58587.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1       1
FT   NON_TER     116     116
SQ   SEQUENCE   116 AA;  12294 MW;  F7B0E9F49FAE369E CRC64;

  Query Match             29.1%;  Score 191.5;  DB 4;  Length 116;
  Best Local Similarity   41.7%;  Pred. No. 9.7e-14;
  Matches   43;  Conservative   19;  Mismatches   30;  Indels   11;  Gaps    4;

Qy         21 VLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRP 80
              :| |  ::   ||:   :||| |    :   :| | ||| | |||| ::|    ||: ||
Db          3 MLTQPHSVSESPGKTVTISCTGSSGSIA-TNY-VQWYQLRPGSAPTTVIY----EDNQRP 56

Qy         81 ADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC-----SVG 118
              : :||||| : | : |:  |||| :: ||:|||||     |:|
Db         57 SGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSIG 99


RESULT 7
Q96E61
ID   Q96E61      PRELIMINARY;      PRT;   236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   PIR; S12440; S12440.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;

  Query Match             29.0%;  Score 190.5;  DB 4;  Length 236;
  Best Local Similarity   42.0%;  Pred. No. 3e-13;
  Matches   42;  Conservative   21;  Mismatches   30;  Indels    7;  Gaps    3;
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Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              | :|:|||| ::  ||| :||| | ::  | | |||| |:||: |:|
Db         17 SWAQSVLAQPPSVSGAPGQTVTISCTGSSTNIG-AGYAVHWYQQFPGAAPKVLIY----G 71

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              :::||: :||||| :|  :  :  | |: :| ||:|||||
Db         72 NYNRPSGVPDRFSGSK--SGTSASLAITGLQAEDEADYYC 109


RESULT 8
Q8WTU6
ID   Q8WTU6      PRELIMINARY;      PRT;   237 AA.
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24884 MW;  E6CF371E753968E8 CRC64;

  Query Match             28.5%;  Score 187;  DB 4;  Length 237;
  Best Local Similarity   41.1%;  Pred. No. 7.5e-13;
  Matches   44;  Conservative   20;  Mismatches   35;  Indels    8;  Gaps    4;

Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              | :|:|| |  ::  |||  :||| | ::  | | |||| |:||: |:|  |
Db         17 SWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIG-AGYDVHWYQQLPGTAPKLLIYGNS-- 73

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFS 122
                :||: :||||| :|  :  :  | |: :| ||:|||||   | :|
Db         74 --NRPSGVPDRFSGSK--SGTSASLAITGLQAEDEADYYCQ-SYDYS 115


RESULT 9
Q8WUK4
ID   Q8WUK4      PRELIMINARY;      PRT;   237 AA.
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   PIR; S12441; S12441.
DR   PIR; S12627; S12627.
DR   PIR; S29258; S29258.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24897 MW;  73C7D70B8039D186 CRC64;

  Query Match             28.1%;  Score 184.5;  DB 4;  Length 237;
  Best Local Similarity   42.0%;  Pred. No. 1.4e-12;
  Matches   42;  Conservative   19;  Mismatches   32;  Indels    7;  Gaps    3;

Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              | :|:|| |  ::  |||  :||| |  ::  | | ||||  |:||: |:|  |
Db         17 SWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIG-AGYDVHWYQQLPGTAPKLLIYGNS-- 73

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
                :||: :||||| :|  :  :  | |: :| ||:|||||
Db         74 --NRPSGVPDRFSGSK--SGTSASLAITGLQAEDEADYYC 109


RESULT 10
Q8WUK3
ID   Q8WUK3      PRELIMINARY;      PRT;   240 AA.
AC   Q8WUK3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020236; AAH20236.1; -.
DR   PIR; S16439; S16439.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   240 AA;  25977 MW;  921E47DDCA7259F0 CRC64;

  Query Match             27.7%;  Score 182;  DB 4;  Length 240;
  Best Local Similarity   33.9%;  Pred. No. 2.8e-12;
  Matches   43;  Conservative   24;  Mismatches   44;  Indels   16;  Gaps    4;

Qy          6 LSFLLMGTFLSV---SQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG 62
              :|| |:    |    :  || |  :   | |   :|:|||| :|     | : |||| |
Db          4 VSFYLLPFIFSTGLCALPVLTQPPSASAFLGASIKLTCTLSREH---SSYTIEWYQQRPG 60

Qy         63 SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC------- 115
              :|:|::  :|:  |::  |||| :   |     ||:| :| :|:|:|:|
Db         61 RSPQYIMKVKSDGSHNKGDGIPDRFMGSSSGADR--YLTLSNLQSDDEAEYHCGESHTID 118

Qy        116 -SVGYGF 121
               ||: |
Db        119 GQVGWVF 125


RESULT 11
Q8N355
ID   Q8N355      PRELIMINARY;      PRT;   234 AA.
AC   Q8N355;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
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DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028090; AAH28090.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  24792 MW;  CC848CAEBA4A9D63 CRC64;

  Query Match             27.1%;  Score 178;  DB 4;  Length 234;
  Best Local Similarity   38.9%;  Pred. No. 7.6e-12;
  Matches   44;  Conservative   18;  Mismatches   37;  Indels   14;  Gaps    4;

Qy          9 LLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSA 64
              ||:|       ||:  || |  :: | ||| |:::|  :     |    | ||||: | |
Db          6 LLLGLLSHCTGSVTSYVLTQPPSVSVAPGQTARITCGGN----NIGSKSVHWYQQKPGQA 61

Qy         65 PRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSV 117
              |  ::|    :|  ||: ||:||| :   : |   |||| |   |:||||| :
Db         62 PVLVVY----DDSDRPSGIPERFSGS--NSGNTATLTISRVDAGDEADYYCQL 108


RESULT 12
Q99M11
ID   Q99M11      PRELIMINARY;      PRT;   235 AA.
AC   Q99M11;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002129; AAH02129.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25403 MW;  39807BFE6782A3FB CRC64;

  Query Match             26.5%;  Score 174;  DB 11;  Length 235;
  Best Local Similarity   40.0%;  Pred. No. 2.2e-11;
  Matches   40;  Conservative   16;  Mismatches   38;  Indels    6;  Gaps    2;

Qy         16 SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEE 75
              | :| || |  ::    |  |:| |  |  :  | |  |:|||  | :|  ::|
Db         17 SCAQLVLTQPSSVSTSLGSTAKLPCKASTGN--IGDSYVNWYQQYMGRSPTNMIY----G 70

Qy         76 DHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              |  ||: : |||| : | : |:  |||  || :|:|||||
Db         71 DDLRPSGVSDRFSGSIDSSSNSAFLTIQNVQADDEADYYC 110


RESULT 13
Q9NSD6
ID   Q9NSD6      PRELIMINARY;      PRT;   107 AA.
AC   Q9NSD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Hohmann A.;
RT   "Autoimmunity.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11306 MW;  A2B04B37187A5F00 CRC64;

  Query Match             26.0%;  Score 171;  DB 4;  Length 107;
  Best Local Similarity   40.0%;  Pred. No. 1.8e-11;
  Matches   38;  Conservative   18;  Mismatches   29;  Indels   10;  Gaps    3;

Qy         22 LAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPA 81
              | |   : |  ||  :::|     |  ::| |  |||||: | ||  ::| :    ::||:
Db          2 LTQDPVVSVALGQTVRITC----QGDSLRSYYASWYQQKPGQAPVLVIYGK----NNRPS 53

Qy         82 DIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCS 116
              |||||| :   : |    |||:  | ||:|||||:
Db         54 GIPDRFSGS--SSGNTASLTITGAQAEDEADYYCN 86


RESULT 14
Q8TBC9
ID   Q8TBC9      PRELIMINARY;      PRT;   233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022823; AAH22823.1; -.
DR   PIR; S12442; S12442.
DR   PIR; S30526; S30526.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24867 MW;  367411BFD6F4DF92 CRC64;

  Query Match           25.9%;  Score 170;  DB 4;  Length 233;
  Best Local Similarity  40.2%;  Pred. No. 6.1e-11;
  Matches   39;  Conservative   17;  Mismatches   25;  Indels   16;  Gaps    4;

Qy         22 LAQLDALLVFPGQVAQLSCT---LSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHH 78
              | |  :: | ||| |:::|:   |  |:         ||||: | ||  ::|    :|:
Db         23 LTQPPSVSVSPGQTARITCSGDALPKQY-------AYWYQQKPGQAPVLVIY----KDNE 71

Qy         79 RPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYC 115
              ||: ||:||| :   :     |||| || ||:|||||
Db         72 RPSGIPERFSGS--SSGTTVTLTISGVQAEDEADYYC 106


RESULT 15
Q7Z2U7
ID   Q7Z2U7      PRELIMINARY;      PRT;   234 AA.
AC   Q7Z2U7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054883; AAH54883.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  25015 MW;  9A5723ABC393A06F CRC64;

  Query Match           25.9%;  Score 170;  DB 4;  Length 234;
  Best Local Similarity  36.3%;  Pred. No. 6.1e-11;
  Matches   41;  Conservative   22;  Mismatches   36;  Indels   14;  Gaps    4;

Qy          9 LLMGTFL----SVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSA 64
              ||:|       ||:  || |  :: | ||: |:::|        |    | ||||:   |
Db          6 LLLGLLSHCTDSVASYVLTQPPSVSVAPGKTARITCGAD----NIGAKSVHWYQQKTDQA 61

Qy         65 PRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSV 117
                 | :::    :|: ||: ||:||| :   : |   |:|| |:| |:|||:| |
Db         62 PVLVVH----DDNDRPSGIPERFSGS--NSGNTATLSISRVEPGDEADYFCQV 108


Search completed: June 28, 2004, 08:27:58
Job time : 41.4459 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:28:50 ; Search time 43.7703 Seconds
(without alignments)
793.337 Million cell updates/sec

Title: US-09-981-876-200
Perfect score: 657
Sequence: 1 MACRCLSFLLMGTFLSVSQT.....PVQPEDDADYYCSVGYGFSP 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	657	100.0	123	9	US-09-989-722-117	Sequence 117, App
2	657	100.0	123	9	US-09-989-723-117	Sequence 117, App
3	657	100.0	123	9	US-09-989-279-117	Sequence 117, App
4	657	100.0	123	9	US-09-989-727-117	Sequence 117, App
5	657	100.0	123	9	US-09-989-731-117	Sequence 117, App
6	657	100.0	123	9	US-09-989-732-117	Sequence 117, App
7	657	100.0	123	9	US-09-991-073-117	Sequence 117, App
8	657	100.0	123	9	US-09-990-442-117	Sequence 117, App
9	657	100.0	123	9	US-09-991-163-117	Sequence 117, App
10	657	100.0	123	9	US-09-993-604-117	Sequence 117, App
11	657	100.0	123	9	US-09-990-456-117	Sequence 117, App
12	657	100.0	123	9	US-09-989-721-117	Sequence 117, App
13	657	100.0	123	9	US-09-992-598-117	Sequence 117, App
14	657	100.0	123	9	US-09-981-876-200	Sequence 200, App
15	657	100.0	123	9	US-09-989-293A-117	Sequence 117, App
16	657	100.0	123	9	US-09-989-735-117	Sequence 117, App
17	657	100.0	123	9	US-09-990-444-117	Sequence 117, App
18	657	100.0	123	9	US-09-991-181-117	Sequence 117, App
19	657	100.0	123	9	US-09-989-730-117	Sequence 117, App
20	657	100.0	123	9	US-09-990-436-117	Sequence 117, App
21	657	100.0	123	9	US-09-993-687-117	Sequence 117, App
22	657	100.0	123	10	US-09-989-734-117	Sequence 117, App
23	657	100.0	123	10	US-09-997-653-117	Sequence 117, App
24	657	100.0	123	10	US-09-993-667-117	Sequence 117, App
25	657	100.0	123	10	US-09-148-545-200	Sequence 200, App
26	657	100.0	123	10	US-09-997-428-117	Sequence 117, App
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31	657	100.0	123	10	US-09-989-726-117	Sequence 117, App
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36	657	100.0	123	10	US-09-997-573-117	Sequence 117, App
37	657	100.0	123	10	US-09-991-172-117	Sequence 117, App
38	657	100.0	123	10	US-09-990-726-117	Sequence 117, App
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40	657	100.0	123	10	US-09-997-601-117	Sequence 117, App
41	657	100.0	123	10	US-09-990-443-117	Sequence 117, App
42	657	100.0	123	10	US-09-991-854-117	Sequence 117, App
43	657	100.0	123	10	US-09-997-628-117	Sequence 117, App
44	657	100.0	123	10	US-09-997-683-117	Sequence 117, App
45	657	100.0	123	10	US-09-989-729A-117	Sequence 117, App

ALIGNMENTS

RESULT 1
US-09-989-722-117
; Sequence 117, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
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; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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RESULT 3
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; Patent No. US20020072496A1
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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 FSP 123
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RESULT 4
US-09-989-727-117
; Sequence 117, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 117, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-11-20

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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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RESULT 6
US-09-989-732-117
; Sequence 117, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
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Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C15

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; Patent No. US20020132252A1
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
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; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        121 FSP 123
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RESULT 9
US-09-991-163-117
; Sequence 117, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
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RESULT 10
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; Sequence 117, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 657; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 3e-64;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
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; Sequence 117, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 657; DB 9; Length 123;
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Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; APPLICANT: Baker,Kevin P.
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; APPLICANT: Zhang, Zemin
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RESULT 14
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
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; CURRENT FILING DATE: 2001-10-19
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Best Local Similarity 100.0%; Pred. No. 3e-64;
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; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
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; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Zhang, Zemin
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	657	100.0	123	21	US-09-709-238-117	Sequence 117, App
5	657	100.0	123	22	US-09-791-537-2522	Sequence 2522, Ap
6	657	100.0	123	23	US-09-834-366-18461	Sequence 18461, A
7	657	100.0	123	24	US-09-941-992-117	Sequence 117, App
8	657	100.0	123	25	US-09-964-994A-117	Sequence 117, App
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11	657	100.0	123	25	US-09-989-293A-117	Sequence 117, App
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28	657	100.0	123	25	US-09-989-862-117	Sequence 117, App
29	657	100.0	123	25	US-09-990-427-117	Sequence 117, App
30	657	100.0	123	25	US-09-990-436-117	Sequence 117, App
31	657	100.0	123	25	US-09-990-437-117	Sequence 117, App
32	657	100.0	123	25	US-09-990-438-117	Sequence 117, App
33	657	100.0	123	25	US-09-990-439-117	Sequence 117, App
34	657	100.0	123	25	US-09-990-440-117	Sequence 117, App
35	657	100.0	123	25	US-09-990-441-117	Sequence 117, App
36	657	100.0	123	25	US-09-990-442-117	Sequence 117, App
37	657	100.0	123	25	US-09-990-443-117	Sequence 117, App
38	657	100.0	123	25	US-09-990-444-117	Sequence 117, App
39	657	100.0	123	25	US-09-990-456-117	Sequence 117, App
40	657	100.0	123	25	US-09-990-562-117	Sequence 117, App
41	657	100.0	123	25	US-09-990-711-117	Sequence 117, App
42	657	100.0	123	25	US-09-990-726-117	Sequence 117, App
43	657	100.0	123	25	US-09-991-073-117	Sequence 117, App
44	657	100.0	123	25	US-09-991-150-117	Sequence 117, App
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ALIGNMENTS

RESULT 1
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; Sequence 402, Application PC/TUS0143523
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

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;  FILE REFERENCE: P3330R1C331
;  CURRENT APPLICATION NUMBER: PCT/US01/43523
;  CURRENT FILING DATE:  2002-10-02
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 402
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo Sapien
PCT-US01-43523-402

  Query Match            100.0%;  Score 657;  DB 1;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-65;
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Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

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Db        121 FSP 123


RESULT 2
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; Sequence 402, Application PC/TUS0224563
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C331
;  CURRENT APPLICATION NUMBER: PCT/US02/24563
;  CURRENT FILING DATE:  2002-08-02
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
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;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 402
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo Sapien
PCT-US02-24563-402

  Query Match            100.0%;  Score 657;  DB 1;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-65;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123


RESULT 3
US-09-621-011-200
; Sequence 200, Application US/09621011
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 70 Human Secreted Proteins
;  FILE REFERENCE: PZ001P1
;  CURRENT APPLICATION NUMBER: US/09/621,011
;  CURRENT FILING DATE:  2000-07-20
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 280
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-621-011-200

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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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Db        121 FSP 123


RESULT 4
US-09-709-238-117
; Sequence 117, Application US/09709238
; GENERAL INFORMATION:
;  APPLICANT:  Baker, Kevin
;  APPLICANT:  Chen, Jian
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Yuan, Jean
;  TITLE OF INVENTION:  Novel Polypeptides and Nucleic Acids Encoding the Same
;  FILE REFERENCE:  P2730R1C1
;  CURRENT APPLICATION NUMBER: US/09/709,238
;  CURRENT FILING DATE:  2000-11-08
;  PRIOR APPLICATION NUMBER:  PCT/US99/12252
;  PRIOR FILING DATE:  1999-06-02
;  PRIOR APPLICATION NUMBER:  US 60/087,607
;  PRIOR FILING DATE:  1998-06-02
;  PRIOR APPLICATION NUMBER:  US 60/087,609
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;  PRIOR APPLICATION NUMBER:  US 60/088,025
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;  PRIOR APPLICATION NUMBER:  US 60/088,028
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;  PRIOR APPLICATION NUMBER:  US 60/088,029
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;  PRIOR APPLICATION NUMBER:  US 60/091,360
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;  PRIOR APPLICATION NUMBER:  US 60/091,519
;  PRIOR FILING DATE:  1998-07-02
;  PRIOR APPLICATION NUMBER:  US 60/091,544
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;  PRIOR APPLICATION NUMBER:  US 60/091,628
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;  PRIOR APPLICATION NUMBER:  US 60/091,646
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;  PRIOR APPLICATION NUMBER:  US 60/091,978
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;  PRIOR FILING DATE:  1998-07-10
;  PRIOR APPLICATION NUMBER:  US 60/093,339
;  PRIOR FILING DATE:  1998-07-20
;  PRIOR APPLICATION NUMBER:  US 60/094,651
;  PRIOR FILING DATE:  1998-07-30

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123


RESULT 5
US-09-791-537-2522
; Sequence 2522, Application US/09791537
; GENERAL INFORMATION:
;  APPLICANT: Bionomix, Inc.
;  APPLICANT:  Debe, Derek
;  APPLICANT:  Danzer, Joseph
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
;  TITLE OF INVENTION:  METHODS OF USE THEREOF
;  FILE REFERENCE: 261/210
;  CURRENT APPLICATION NUMBER: US/09/791,537
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 153055
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2522
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-791-537-2522

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

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RESULT 6
US-09-834-366-18461
; Sequence 18461, Application US/09834366
; GENERAL INFORMATION:
;  APPLICANT: Bejanin, Stephane
;  APPLICANT:  Tanaka, Hiroaki
;  APPLICANT:  Dumas Milne Edwards, Jean Baptiste
;  APPLICANT:  Jobert, Severin
;  APPLICANT:  Giordano, Jean-Yves
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: 81.US2.REG
;  CURRENT APPLICATION NUMBER: US/09/834,366
;  CURRENT FILING DATE:  2001-04-13
;  PRIOR APPLICATION NUMBER: US 60/197,873
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 52153
;  SOFTWARE: Patent.pm
; SEQ ID NO 18461
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: -20..-1
US-09-834-366-18461

  Query Match             100.0%;  Score 657;  DB 23;  Length 123;
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  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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US-09-941-992-117
; Sequence 117, Application US/09941992
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C1
;  CURRENT APPLICATION NUMBER: US/09/941,992
;  CURRENT FILING DATE:  2001-08-28
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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RESULT 8
US-09-964-994A-117
; Sequence 117, Application US/09964994A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/964,994A
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US/09/941,992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 532
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;   LENGTH: 123
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US-09-964-994A-117

  Query Match             100.0%;  Score 657;  DB 25;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-65;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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Db        121 FSP 123


RESULT 9
US-09-981-876-200
; Sequence 200, Application US/09981876
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 70 Human Secreted Proteins
;  FILE REFERENCE: PZ001P1
;  CURRENT APPLICATION NUMBER: US/09/981,876
;  CURRENT FILING DATE:  2001-10-19
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; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 123
; TYPE: PRT

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 10
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; Sequence 117, Application US/09989279
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 657; DB 25; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 11
US-09-989-293A-117
; Sequence 117, Application US/09989293A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 657; DB 25; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 12
US-09-989-328-117
; Sequence 117, Application US/09989328
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C54
; CURRENT APPLICATION NUMBER: US/09/989,328
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322

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;  PRIOR FILING DATE: 1998-04-28
;  PRIOR APPLICATION NUMBER: 60/084600
;  PRIOR FILING DATE: 1998-05-07
;  PRIOR APPLICATION NUMBER: 60/087106
;  PRIOR FILING DATE: 1998-05-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 117
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-989-328-117

  Query Match             100.0%;  Score 657;  DB 25;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-65;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
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Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
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Db        121 FSP 123


RESULT 13
US-09-989-721-117
; Sequence 117, Application US/09989721
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C55
;  CURRENT APPLICATION NUMBER: US/09/989,721
;  CURRENT FILING DATE:  2001-11-19
;  PRIOR APPLICATION NUMBER: 60/049787
;  PRIOR FILING DATE: 1997-06-16
;  PRIOR APPLICATION NUMBER: 60/062250
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/065186
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Query Match 100.0%; Score 657; DB 25; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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Db        121 FSP 123
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RESULT 14
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; Sequence 117, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 100.0%; Score 657; DB 25; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
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Qy        121 FSP 123
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RESULT 15
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; GENERAL INFORMATION:
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; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
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; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 657; DB 25; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-65;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQR 60

Qy         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYG 120

Qy        121 FSP 123
              |||
Db        121 FSP 123
```

Search completed: June 28, 2004, 08:36:06
Job time : 198.243 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:35 ; Search time 12.0405 Seconds
(without alignments)
790.908 Million cell updates/sec

Title: US-09-981-876-200_COPY_25_123
Perfect score: 538
Sequence: 1 LDALLVFPGQVAQLSCTLSP.....PVQPEDDADYYCSVGYGFSP 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	372.5	69.2	123	2	S35302	B-cell protein 8HS
2	233.5	43.4	142	2	B28344	VpreB protein prec
3	229.5	42.7	142	2	A28344	VpreB protein prec
4	207.5	38.6	139	2	S00258	VpreB protein - hu
5	207.5	38.6	145	2	I57832	VPre-B protein - h
6	200	37.2	111	1	L6HUST	Ig lambda chain V-
7	197	36.6	112	1	L6HUAR	Ig lambda chain V-
8	192.5	35.8	232	2	S17399	Ig lambda chain pr
9	191.5	35.6	243	2	S25755	Ig lambda chain -
10	189.5	35.2	120	2	PS0055	Ig lambda chain pr
11	185.5	34.5	99	2	S36058	Ig lambda chain -
12	185.5	34.5	111	1	L2HUMC	Ig lambda chain V-
13	185	34.4	111	1	L6HULT	Ig lambda chain V-
14	184.5	34.3	120	2	PS0056	Ig lambda chain pr
15	184.5	34.3	136	2	S16848	Ig lambda chain V-
16	183.5	34.1	118	2	A32529	Ig lambda chain pr
17	183	34.0	131	1	L6HUEB	Ig lambda chain pr
18	182.5	33.9	133	2	A28565	Ig lambda chain pr
19	182.5	33.9	216	2	S69130	Ig lambda chain (D
20	181.5	33.7	99	2	S36057	Ig lambda chain -
21	180.5	33.6	98	2	S36068	Ig lambda chain -
22	180.5	33.6	111	1	L2HUBO	Ig lambda chain V-
23	180.5	33.6	117	2	S04525	Ig lambda chain pr
24	180	33.5	107	2	B46516	Ig lambda chain V
25	178.5	33.2	235	2	S25758	Ig lambda chain -
26	176.5	32.8	94	2	C32529	Ig lambda chain V
27	176.5	32.8	111	2	S46397	Ig lambda chain V
28	176.5	32.8	112	2	S31515	Ig lambda chain V
29	176	32.7	108	2	S38498	Ig lambda chain -
30	175.5	32.6	99	2	S36051	Ig lambda chain -
31	175.5	32.6	106	2	S40091	Ig light chain - m
32	175.5	32.6	112	1	L2HUNG	Ig lambda chain V-
33	175.5	32.6	234	2	A39956	Ig lambda chain pr
34	175	32.5	111	1	L2HUWN	Ig lambda chain V-
35	174.5	32.4	99	2	S36056	Ig lambda chain -
36	173.5	32.2	111	2	S19673	Ig lambda chain V
37	173.5	32.2	132	2	A55410	Ig light chain V r
38	173	32.2	112	2	D44151	Ig lambda chain V
39	173	32.2	113	2	A29700	Ig lambda chain V
40	172.5	32.1	99	2	S36052	Ig lambda chain -
41	172.5	32.1	99	2	S36053	Ig lambda chain -
42	172.5	32.1	109	1	L2HUBR	Ig lambda chain V-
43	172.5	32.1	112	2	S51148	antibody light cha
44	172.5	32.1	118	2	S12627	Ig lambda chain pr
45	171.5	31.9	110	2	S57412	Ig lambda chain V-

ALIGNMENTS

RESULT 1
S35302
B-cell protein 8HS-20 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 20-Jun-2000
C;Accession: S35302
R;Shirasawa, T.; Ohnishi, K.; Hagiwara, S.; Shigemoto, K.; Takebe, Y.; Rajewsky, K.; Ta
EMBO J. 12, 1827-1834, 1993
A;Title: A novel gene product associated with mu chains in immature B cells.
A;Reference number: S35302; MUID:93259124; PMID:8491176
A;Accession: S35302
A;Molecule type: DNA
A;Residues: 1-123 <SHI>
A;Cross-references: EMBL:D13208; NID:g286064; PIDN:BAA02495.1; PID:g286065
C;Genetics:
A;Gene: 8HS-20
A;Introns: 18/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: B-cell
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-123/Product: B-cell protein 8HS-20 #status predicted <MAT>

Query Match 69.2%; Score 372.5; DB 2; Length 123;
Best Local Similarity 69.4%; Pred. No. 2.3e-31;
Matches 68; Conservative 11; Mismatches 18; Indels 1; Gaps 1;

```
Qy          2 DALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPD 61
              ||  ||||| | ||||:: || |  | |||||||: |||| :|||| :|||:|:|||||||
Db         27 DAFSVFPGQDAHLSCTINSQHATAGDIGVSWYQQQPGSAP-HLLYYYAEEEHYRPADIPD 85

Qy         62 RFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              ||||  | |||||:|||||| |||||||:||: : | |
Db         86 RFSATVDAAHNACILTISPVLPEDDADYFCSIAHTFEP 123
```

RESULT 2
B28344
VpreB protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 05-Nov-1999
C;Accession: B28344
R;Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be s
A;Reference number: A91077; MUID:88029315; PMID:3117530
A;Accession: B28344
A;Molecule type: DNA
A;Residues: 1-142 <KUD>
A;Cross-references: GB:X05563; GB:Y00079; NID:g55415; PIDN:CAA29077.1; PID:g55416
A;Note: the authors translated the codon GAG for residue 110 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;20-142/Product: VpreB protein #status predicted <MAT>

Query Match 43.4%; Score 233.5; DB 2; Length 142;
Best Local Similarity 54.7%; Pred. No. 5.8e-17;
Matches 47; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

```
Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :||||||  |  |  | : |||||  |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                | |   |:|| :||||:| |||:||
Db         93 TARNLGYLSISELQPEDEAVYYCAVG 118
```

RESULT 3
A28344
VpreB protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000
C;Accession: A28344
R;Kudo, A.; Melchers, F.
EMBO J. 6, 2267-2272, 1987
A;Title: A second gene, VpreB in the lambda-5 locus of the mouse, which appears to be se
A;Reference number: A91077; MUID:88029315; PMID:3117530
A;Accession: A28344
A;Molecule type: DNA
A;Residues: 1-142 <KUD>
A;Cross-references: GB:X05556; GB:Y00079; NID:g55409; PIDN:CAA29071.1; PID:g55410
A;Note: the authors translated the codon GAG for residue 110 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;20-142/Product: VpreB1 protein #status predicted <MAT>

Query Match 42.7%; Score 229.5; DB 2; Length 142;
Best Local Similarity 53.5%; Pred. No. 1.5e-16;
Matches 46; Conservative 9; Mismatches 30; Indels 1; Gaps 1;

```
Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :||||||  |  |  | : |||||  |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                |   |:|| :||||:| |||:||
Db         93 TTRNLGYLSISELQPEDEAVYYCAVG 118
```

RESULT 4
S00258
VpreB protein - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Nov-1999
C;Accession: S00258
R;Bauer, S.R.; Kudo, A.; Melchers, F.
EMBO J. 7, 111-116, 1988
A;Title: Structure and pre-B lymphocyte restricted expression of the VpreB gene in human
A;Reference number: S00258; MUID:88196069; PMID:3258819
A;Accession: S00258
A;Molecule type: DNA
A;Residues: 1-139 <BAU>
A;Cross-references: EMBL:M34927; NID:g340304; PIDN:AAA61292.1; PID:g340305
C;Genetics:
A;Gene: GDB:VPREB1
A;Cross-references: GDB:120493; OMIM:146770
A;Map position: 22q11.2-22q11.2
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 38.6%; Score 207.5; DB 2; Length 139;
Best Local Similarity 48.8%; Pred. No. 2.7e-14;
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

```
Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :|:|||   |  |  | | ||||| |  ||:|| | |:  |  :   :| ||| :||
Db         34 GTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKSQGPQVPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                | |   |:|| :||||:| |||::|
Db         93 VARNRGYLSISELQPEDEAMYYCAMG 118
```

RESULT 5
I57832
VPre-B protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I57832
R;Guelpa-Fonlupt, V.; Bossy, D.; Alzari, P.; Fumoux, F.; Fougereau, M.; Schiff, C.
Mol. Immunol. 31, 1099-1108, 1994
A;Title: The human pre-B cell receptor: structural constraints for a tentative model of
A;Reference number: I57832; MUID:95021318; PMID:7935499
A;Accession: I57832
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <RES>
A;Cross-references: GB:S74019; NID:g693810; PIDN:AAB32118.1; PID:g693811
C;Genetics:
A;Gene: Vpre-B
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 38.6%; Score 207.5; DB 2; Length 145;
Best Local Similarity 48.8%; Pred. No. 2.8e-14;
Matches 42; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

```
Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :|:|||   |  |  | | ||||| |  ||:|| | |:  |  :   :| ||| :||
Db         34 GTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKSQGPQVPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                | |   |:|| :||||:| |||::|
Db         93 VARNRGYLSISELQPEDEAMYYCAMG 118
```

RESULT 6
L6HUST
Ig lambda chain V-VI region (SUT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01988
R;Solomon, A.; Kyle, R.A.; Frangione, B.
in Amyloidosis, Glenner, G.G., Osserman, E.F., Benditt, E.P., Calkins, E., Cohn, A.S., a
A;Title: Light chain variable region subgroups of monoclonal immunoglobulins in amyloido
A;Reference number: A01988
A;Accession: A01988
A;Molecule type: protein
A;Residues: 1-111 <SOL>
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-100/Region: complementarity-determining 3
F;101-111/Region: framework 4
F;22-91/Disulfide bonds: #status predicted

Query Match 37.2%; Score 200; DB 1; Length 111;
Best Local Similarity 48.8%; Pred. No. 1.2e-13;
Matches 41; Conservative 12; Mismatches 25; Indels 6; Gaps 2;

```
Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :||| |    ||  | | ||||| | ||  :::    ||  ||: :||||| :
Db         14 PGKTVIISCTRSDG--TIAGYYVQWYQQRPGRAPTTVIF----EDTQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :| ||:|||||
Db         68 DRSSNSASLTISGLQTEDEADYYC 91


RESULT 7
L6HUAR
Ig lambda chain V-VI region (AR) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
C;Accession: A01987
R;Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.
Biochem. J. 195, 561-572, 1981
A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-cha
A;Reference number: A01987; MUID:82091000; PMID:6797401
A;Contents: amyloid protein AR
A;Accession: A01987
A;Molecule type: protein
A;Residues: 1-112 <SLE>
A;Note: about half of the lambda chain C region is missing from this protein
C;Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
F;22-91/Disulfide bonds: #status predicted

  Query Match             36.6%;  Score 197;  DB 1;  Length 112;
  Best Local Similarity   47.6%;  Pred. No. 2.6e-13;
  Matches   40;  Conservative   15;  Mismatches   23;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:    ||| |    :| |  | ||||| |||| ::|    :|: ||: :||||| :
Db         14 PGKTVTFSCTGSGG--SIADSFVQWYQQRPGSAPTTVIY----DDNQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              |:: |:  |||| :: ||:|||||
Db         68 DDSANSASLTISGLKTEDEADYYC 91


RESULT 8
S17399
Ig lambda chain precursor - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17399
R;Hayzer, D.J.; Young-Cooper, G.O.; Mage, R.G.; Jaton, J.C.
Eur. J. Immunol. 20, 2707-2712, 1990
A;Title: cDNA clones encoding immunoglobulin lambda chains from rabbit expressing the ph
A;Reference number: S17399; MUID:91099420; PMID:2125274
A;Accession: S17399
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <HAY>
A;Cross-references: EMBL:X57729; NID:g1593; PIDN:CAA40896.1; PID:g1594
A;Note: the authors translated the codon TTA for residue 92 as Trp and AGC for residue 1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;147-215/Domain: immunoglobulin homology <IMM>

  Query Match             35.8%;  Score 192.5;  DB 2;  Length 232;
  Best Local Similarity   43.7%;  Pred. No. 1.7e-12;
  Matches   38;  Conservative   14;  Mismatches   30;  Indels    5;  Gaps    2;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |  |:|:|||| | |   | : ||||: | |||||:: :|:  : :   :||||| :
Db         30 GASARLTCTLSSAHKT---YTIDWYQQQQGEAPRYLMHIKSDGSYTKGTGVPDRFSGSSS 86

Qy         69 EAHNACVLTISPVQPEDDADYYCSVGY 95
              |      | |   || :|:|||||   |
Db         87 GADR--YLIIPSVQADDEADYYCGADY 111


RESULT 9
S25755
Ig lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S25755
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin la
A;Reference number: S16439; MUID:91257162; PMID:1904362
A;Accession: S25755
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-243 <COM>
A;Cross-references: EMBL:X57820; NID:g33739; PIDN:CAA40957.1; PID:g33740
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;158-226/Domain: immunoglobulin homology <IMM>

  Query Match             35.6%;  Score 191.5;  DB 2;  Length 243;
  Best Local Similarity   41.1%;  Pred. No. 2.2e-12;
  Matches   37;  Conservative   19;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :|:| ||    :: |: : ||||: |: |||||||| |: :  : : :| ||| : |
Db         34 GASVRLTCMLS-SGFSVGDFWIRWYQQKPGNPPRYLLYYHSDSNKGQGSGVPSRFSGSND 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVGYGFS 98
              : || :| || :| | :|||||   :  |
Db         93 ASANAGILRISGLQLEVEADYYCGTWHSNS 122


RESULT 10
PS0055
Ig lambda chain precursor V-II region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C;Accession: PS0055
R;Hayzer, D.J.; Jaton, J.C.
Gene 80, 185-191, 1989
A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lam
A;Reference number: A91614; MUID:90006781; PMID:2507399
A;Accession: PS0055
A;Molecule type: DNA
A;Residues: 1-120 <HAY>
A;Cross-references: GB:M27840; NID:g341760; PIDN:AAA31363.1; PID:g552407
A;Note: the authors translated the codon TTG for residue 97 as Trp
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig lambda chain V-II region #status predicted <MAT>

  Query Match             35.2%;  Score 189.5;  DB 2;  Length 120;
  Best Local Similarity   43.7%;  Pred. No. 1.6e-12;
  Matches   38;  Conservative   13;  Mismatches   31;  Indels    5;  Gaps    2;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |  |:|:|||| | |   | : ||||: | |||||:  :|:  : :   :||||| :
Db         35 GASAKLTCTLSSAHKT---YTIDWYQQQQGEAPRYLMQLKSDGSYTKGTGVPDRFSGSSS 91

Qy         69 EAHNACVLTISPVQPEDDADYYCSVGY 95
```

```
                |     | |  || :|:|||||   |
Db          92 GADR--YLIIPSVQADDEADYYCGADY 116


RESULT 11
S36058
Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 23-Jul-1999
C;Accession: S36058
R;Williams, S.C.
submitted to the EMBL Data Library, April 1993
A;Reference number: S36046
A;Accession: S36058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <WIL>
A;Cross-references: EMBL:Z22199; NID:g312858; PIDN:CAA80209.1; PID:g312859
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             34.5%;  Score 185.5;  DB 2;  Length 99;
  Best Local Similarity   46.7%;  Pred. No. 3.4e-12;
  Matches   42;  Conservative   13;  Mismatches   20;  Indels   15;  Gaps    4;

Qy           8 PGQVAQLSCTLSPQHVTIRDYG----VSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRF 63
               |||   :|||     |  | |    ||||||  |:||: ::|    |  :||: :|||| 
Db          14 PGQSVTISCT-----GTSSDVGSYNRVSWYQQPPGTAPKLMIY----EVSNRPSGVPDRF 64

Qy          64 SAAKDEAHNACVLTISPVQPEDDADYYCSV 93
                 | :|  : |   |||| :| ||:||||||: 
Db          65 SGSK--SGNTASLTISGLQAEDEADYYCSL 92


RESULT 12
L2HUMC
Ig lambda chain V-II region (Mcg) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999
C;Accession: A90381; A01975
R;Fett, J.W.; Deutsch, H.F.
Biochemistry 13, 4102-4114, 1974
A;Title: Primary structure of the Mcg lambda chain.
A;Reference number: A90381; MUID:75013804; PMID:4415202
A;Accession: A90381
A;Molecule type: protein
A;Residues: 1-111 <FET>
A;Note: the C region of this chain has the Kern+ and Mcg+ markers
R;Fett, J.W.; Deutsch, H.F.
Immunochemistry 12, 643-652, 1975
A;Title: A new lambda-chain gene.
A;Reference number: A91745; MUID:76093781; PMID:812801
A;Contents: annotation; lambda chain genes
A;Note: the Mcg-type C region appears to be correlated with a very unusual V-region subs
R;Edmundson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.
Biochemistry 14, 3953-3961, 1975
A;Title: Rotational allomerism and divergent evolution of domains in immunoglobulin ligh
A;Reference number: A90391
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-90/Disulfide bonds: #status predicted

  Query Match             34.5%;  Score 185.5;  DB 1;  Length 111;
  Best Local Similarity   47.6%;  Pred. No. 3.9e-12;
  Matches   40;  Conservative   14;  Mismatches   23;  Indels    7;  Gaps    3;

Qy           9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
               ||   :||| :   |   :| |||||| || ||: ::|    | : ||: :||||| :| 
Db          15 GQSVTISCTGTSSDVGGYNY-VSWYQQHAGKAPKVIIY----EVNKRPSGVPDRFSGSK- 68

Qy          69 EAHNACVLTISPVQPEDDADYYCS 92
                 : |   ||:| :| ||:||||||
Db          69 -SGNTASLTVSGLQAEDEADYYCS 91


RESULT 13
L6HULT
Ig lambda chain V-VI region (WLT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01989
R;Dwulet, F.E.; Strako, K.; Benson, M.D.
Scand. J. Immunol. 22, 653-660, 1985
A;Title: Amino acid sequence of a lambda VI primary (AL) amyloid protein (WLT).
A;Reference number: A01989; MUID:86122667; PMID:4089539
A;Accession: A01989
A;Molecule type: protein
A;Residues: 1-111 <DWU>
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Region: framework 1
F;15-93/Domain: immunoglobulin homology <IMM>
F;23-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-57/Region: complementarity-determining 2
F;58-91/Region: framework 3
F;92-101/Region: complementarity-determining 3
F;102-111/Region: framework 4
F;22-91/Disulfide bonds: #status predicted

  Query Match             34.4%;  Score 185;  DB 1;  Length 111;
  Best Local Similarity   45.2%;  Pred. No. 4.4e-12;
  Matches   38;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    2;

Qy           8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
               | :   :||| |     :|     | ||||| ||||  ::|    |:: ||:::||||| :
Db          14 PEKTVTISCTGSSG--SIGSNYVQWYQQRPGSAPTNVIY----ENNQRPSEVPDRFSGSI 67

Qy          68 DEAHNACVLTISPVQPEDDADYYC 91
               | : |:  |||| :: ||:|||||
Db          68 DSSSNSASLTISGLKTEDEADYYC 91


RESULT 14
PS0056
Ig lambda chain precursor V-III region - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-Jul-1999
C;Accession: PS0056
R;Hayzer, D.J.; Jaton, J.C.
Gene 80, 185-191, 1989
A;Title: Cloning and sequencing of two functional rabbit germ-line immunoglobulin V lamb
A;Reference number: A91614; MUID:90006781; PMID:2507399
A;Accession: PS0056
A;Molecule type: DNA
A;Residues: 1-120 <HAY>
A;Cross-references: GB:M27841; NID:g341761; PIDN:AAA31364.1; PID:g552408
A;Note: the authors translated the codon TTG for residue 97 as Trp
C;Genetics:
A;Introns: 17/1
```

```
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-120/Product: Ig lambda chain V-III region #status predicted <MAT>

  Query Match             34.3%;  Score 184.5;  DB 2;  Length 120;
  Best Local Similarity   44.7%;  Pred. No. 5.3e-12;
  Matches   38;  Conservative   13;  Mismatches   29;  Indels    5;  Gaps    2;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |  |:|:||||  | |   | : ||||: | |||||:  :|:  : :   :|||||
Db         35 GSSAKLTCTLSSAHKT---YYIEWYQQQQGEAPRYLMQLKSDGSYTKGTGVPDRFSGSSS 91

Qy         69 EAHNACVLTISPVQPEDDADYYCSV 93
               |     | || || :|:||| | |
Db         92 GADR--YLIISSVQADDEADYICGV 114


RESULT 15
S16848
Ig lambda chain V-II region precursor - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S60297; S16848
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive imm
A;Reference number: S60295; MUID:93122853; PMID:1282498
A;Accession: S60297
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KU2>
A;Cross-references: EMBL:X62125; NID:g38334; PIDN:CAA44056.1; PID:g38335
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>

  Query Match             34.3%;  Score 184.5;  DB 2;  Length 136;
  Best Local Similarity   45.9%;  Pred. No. 6.1e-12;
  Matches   39;  Conservative   14;  Mismatches   25;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   :| |||||   | ||: ::|  ||    ||: :|||||  :|
Db         33 PGQSVTISCTGTSSDVGAYNY-VSWYQHHPGKAPKLMMYEVSE----RPSGVPDRFSGSK 87

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   ||:| :| ||:|||||:
Db         88 --SGNTASLTVSGLQAEDEADYYCT 110


Search completed: June 28, 2004, 08:29:57
Job time : 12.0405 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:35 ; Search time 8.91892 Seconds
(without alignments)
577.979 Million cell updates/sec

Title: US-09-981-876-200_COPY_25_123
Perfect score: 538
Sequence: 1 LDALLVFPGQVAQLSCTLSP.....PVQPEDDADYYCSVGYGFSP 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	538	100.0	123	1	VPR3_HUMAN	Q9uki3 homo sapien
2	233.5	43.4	142	1	VPR2_MOUSE	P13373 mus musculu
3	229.5	42.7	142	1	VPR1_MOUSE	P13372 mus musculu
4	207.5	38.6	145	1	VPRE_HUMAN	P12018 homo sapien
5	200	37.2	111	1	LV6C_HUMAN	P06317 homo sapien
6	197	36.6	112	1	LV6A_HUMAN	P01721 homo sapien
7	185.5	34.5	111	1	LV2F_HUMAN	P01709 homo sapien
8	185	34.4	111	1	LV6D_HUMAN	P06318 homo sapien
9	183	34.0	131	1	LV6E_HUMAN	P06319 homo sapien
10	182.5	33.9	111	1	LV2L_HUMAN	P80422 homo sapien
11	180.5	33.6	111	1	LV2G_HUMAN	P01710 homo sapien
12	175.5	32.6	112	1	LV2K_HUMAN	P04209 homo sapien
13	175	32.5	111	1	LV2I_HUMAN	P01712 homo sapien
14	172.5	32.1	109	1	LV2E_HUMAN	P01708 homo sapien
15	171	31.8	108	1	LV3A_HUMAN	P01714 homo sapien
16	167.5	31.1	110	1	LV2J_HUMAN	P01713 homo sapien
17	167.5	31.1	111	1	LV1D_HUMAN	P01702 homo sapien
18	167	31.0	130	1	LV1G_HUMAN	P06316 homo sapien
19	165	30.7	108	1	LV5A_HUMAN	P01719 homo sapien
20	165	30.7	109	1	LV1F_HUMAN	P04208 homo sapien
21	164	30.5	111	1	LV3B_HUMAN	P80748 homo sapien
22	163.5	30.4	111	1	LV2B_HUMAN	P01705 homo sapien
23	163.5	30.4	111	1	LV2H_HUMAN	P01711 homo sapien
24	162	30.1	106	1	LV4D_HUMAN	P01718 homo sapien
25	161	29.9	106	1	LV4B_HUMAN	P01716 homo sapien
26	161	29.9	109	1	KV3D_HUMAN	P01622 homo sapien
27	160	29.7	107	1	LV4C_HUMAN	P01717 homo sapien
28	160	29.7	108	1	KV3A_HUMAN	P01619 homo sapien
29	159.5	29.6	117	1	LV0A_HUMAN	P04211 homo sapien
30	158	29.4	106	1	LV4A_HUMAN	P01715 homo sapien
31	158	29.4	129	1	KV3L_HUMAN	P18135 homo sapien
32	156	29.0	109	1	KV3B_HUMAN	P01620 homo sapien
33	156	29.0	109	1	KV3G_HUMAN	P04206 homo sapien
34	155.5	28.9	112	1	LV1H_HUMAN	P06887 homo sapien
35	154.5	28.7	111	1	LV2A_HUMAN	P01704 homo sapien
36	154.5	28.7	111	1	LV2C_HUMAN	P01706 homo sapien
37	154.5	28.7	112	1	LV1B_HUMAN	P01700 homo sapien
38	153.5	28.5	111	1	LV2D_HUMAN	P01707 homo sapien
39	153	28.4	111	1	LV1C_HUMAN	P01701 homo sapien
40	152	28.3	112	1	LV6B_HUMAN	P01722 homo sapien
41	152	28.3	129	1	KV3M_HUMAN	P18136 homo sapien
42	148	27.5	100	1	KV3C_HUMAN	P01621 homo sapien
43	147.5	27.4	109	1	KV3E_HUMAN	P01623 homo sapien
44	147	27.3	109	1	LV1I_HUMAN	P06888 homo sapien
45	146	27.1	106	1	LV4E_HUMAN	P06889 homo sapien

ALIGNMENTS

RESULT 1
VPR3_HUMAN
ID VPR3_HUMAN STANDARD; PRT; 123 AA.
AC Q9UKI3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pre-B lymphocyte protein 3 precursor (VpreB3 protein) (N27C7-2).
GN VPREB3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20169186; PubMed=10702669;
RA Rosnet O., Mattei M.-G., Delattre O., Schiff C.;
RT "VPREB3: cDNA characterization and expression in human and chromosome
RT mapping in human and mouse.";
RL Cytogenet. Cell Genet. 87:205-208(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Shimizu N., Minosima S., Kawasaki K., Sasaki T., Hosono K.;
RT "Molecular cloning of N27C7-2 gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS.
CC -!- TISSUE SPECIFICITY: Expressed in B cell precursors. Expressed in
CC fetal liver, bone marrow, spleen and lymph node.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC ---

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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF163825; AAF09451.1; -.
DR   EMBL; AB050772; BAB83034.1; -.
DR   EMBL; BC020666; AAH20666.1; -.
DR   HSSP; P01709; 2MCG.
DR   Genew; HGNC:12710; VPREB3.
DR   MIM; 605017; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    123       PRE-B LYMPHOCYTE PROTEIN 3.
FT   DOMAIN       21    123       IG-LIKE.
FT   DISULFID     40    115       BY SIMILARITY.
SQ   SEQUENCE   123 AA;  13710 MW;  BF09AC5196059E85 CRC64;

  Query Match           100.0%;  Score 538;  DB 1;  Length 123;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-52;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 2
VPR2_MOUSE
ID   VPR2_MOUSE     STANDARD;      PRT;   142 AA.
AC   P13373;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin omega chain precursor (VpreB2 protein).
GN   VPREB2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X DBA/2J;
RX   MEDLINE=88029315; PubMed=3117530;
RA   Kudo A., Melchers F.;
RT   "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT   appears to be selectively expressed in pre-B lymphocytes.";
RL   EMBO J. 6:2267-2272(1987).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X05563; CAA29077.1; -.
DR   PIR; B28344; B28344.
DR   HSSP; P01607; 1REI.
DR   MGD; MGI:98937; Vpreb2.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    142       IMMUNOGLOBULIN OMEGA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
SQ   SEQUENCE   142 AA;  16052 MW;  7EA7128A4E63D920 CRC64;

  Query Match           43.4%;  Score 233.5;  DB 1;  Length 142;
  Best Local Similarity  54.7%;  Pred. No. 9.7e-19;
  Matches   47;  Conservative    9;  Mismatches   29;  Indels    1;  Gaps    1;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :||||||  |  |  | : |||||  |  ||:|| | |  | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
              | |   |:|| :||||:| |||:||
Db         93 TARNLGYLSISELQPEDEAVYYCAVG 118


RESULT 3
VPR1_MOUSE
ID   VPR1_MOUSE     STANDARD;      PRT;   142 AA.
AC   P13372;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin iota chain precursor (VPreB1 protein).
GN   VPREB1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6 X DBA/2J;
RX   MEDLINE=88029315; PubMed=3117530;
RA   Kudo A., Melchers F.;
RT   "A second gene, VpreB in the lambda 5 locus of the mouse, which
RT   appears to be selectively expressed in pre-B lymphocytes.";
RL   EMBO J. 6:2267-2272(1987).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X05556; CAA29071.1; -.
DR   EMBL; X05557; CAA29072.1; -.
```

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DR   PIR; A28344; A28344.
DR   HSSP; P01607; 1REI.
DR   MGD; MGI:98936; Vpreb1.
DR   GO; GO:0005886; C:plasma membrane; IPI.
DR   GO; GO:0004872; F:receptor activity; IPI.
DR   GO; GO:0030097; P:hemopoiesis; IMP.
DR   GO; GO:0006955; P:immune response; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    142       IMMUNOGLOBULIN IOTA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
SQ   SEQUENCE   142 AA;  16125 MW;  2E18BF963A0F448C CRC64;

  Query Match             42.7%;  Score 229.5;  DB 1;  Length 142;
  Best Local Similarity   53.5%;  Pred. No. 2.7e-18;
  Matches   46;  Conservative    9;  Mismatches   30;  Indels    1;  Gaps    1;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :||||||   |   |   | : ||||| |   ||:|| | |   | |:  ||| ||| :||
Db         34 GATIRLSCTLSNDH-NIGIYSIYWYQQRPGHPPRFLLRYFSHSDKHQGPDIPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                 |   |:|| :||||:| |||:||
Db         93 TTRNLGYLSISELQPEDEAVYYCAVG 118


RESULT 4
VPRE_HUMAN
ID   VPRE_HUMAN     STANDARD;      PRT;   145 AA.
AC   P12018;
DT   01-OCT-1989 (Rel. 12, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Immunoglobulin iota chain precursor (V(pre)B protein) (VpreB protein)
DE   (CD179a antigen).
GN   VPREB1 OR VPREB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95021318; PubMed=7935499;
RA   Guelpa-Fonlupt V., Bossy D., Alzari P., Fumoux F., Fougereau M.,
RA   Schiff C.;
RT   "The human pre-B cell receptor: structural constraints for a tentative
RT   model of the pseudo-light (psi L) chain.";
RL   Mol. Immunol. 31:1099-1108(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97228902; PubMed=9074928;
RA   Kawasaki K., Minoshima S., Mine E., Shibuya K., Shintani A.,
RA   Schmeits J.L., Wang J., Shimizu N.;
RT   "One-megabase sequence analysis of the human immunoglobulin lambda
RT   gene locus.";
RL   Genome Res. 7:250-261(1997).
RN   [3]
RP   SEQUENCE OF 1-139 FROM N.A.
RX   MEDLINE=88196069; PubMed=3258819;
RA   Bauer S.R., Kudo A., Melchers F.;
RT   "Structure and pre-B lymphocyte restricted expression of the VpreB in
RT   humans and conservation of its structure in other mammalian
RT   species.";
RL   EMBO J. 7:111-116(1988).
CC   -!- FUNCTION: ASSOCIATES WITH THE IG-MU CHAIN TO FORM A MOLECULAR
CC       COMPLEX THAT IS EXPRESSED ON THE SURFACE OF PRE-B-CELLS. THIS
CC       COMPLEX PRESUMABLY REGULATES IG GENE REARRANGEMENTS IN THE EARLY
CC       STEPS OF B-CELL DIFFERENTIATION.
CC   -!- SUBUNIT: Associates non-covalently with IGLL1.
CC   -!- TISSUE SPECIFICITY: ONLY EXPRESSED BY PRE-B-CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 1:59-63(2000);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/574153212_g.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D86992; BAA19987.1; -.
DR   EMBL; D88270; BAA20030.1; -.
DR   EMBL; S74019; AAB32118.1; -.
DR   EMBL; M34927; AAA61292.1; -.
DR   PIR; I57832; I57832.
DR   PIR; S00258; S00258.
DR   HSSP; P80748; 2LOI.
DR   Genew; HGNC:12709; VPREB1.
DR   MIM; 605141; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Antigen; Signal; Immunoglobulin domain.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    145       IMMUNOGLOBULIN IOTA CHAIN.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     56       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       57     70       FRAMEWORK-2.
FT   DOMAIN       71     81       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       82    115       FRAMEWORK-3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   CONFLICT     10     10       L -> H (IN REF. 3).
SQ   SEQUENCE   145 AA;  16605 MW;  197665B13AF64D46 CRC64;

  Query Match             38.6%;  Score 207.5;  DB 1;  Length 145;
  Best Local Similarity   48.8%;  Pred. No. 7.2e-16;
  Matches   42;  Conservative   12;  Mismatches   31;  Indels    1;  Gaps    1;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |   :|:|||   |   |   | | ||||| |   ||:|| | |: |   :   :| ||| :||
Db         34 GTTIRLTCTLRNDH-DIGVYSVYWYQQRPGHPPRFLLRYFSQSDKSQGPQVPPRFSGSKD 92

Qy         69 EAHNACVLTISPVQPEDDADYYCSVG 94
                | |   |:|| :||||:| |||::|
Db         93 VARNRGYLSISELQPEDEAMYYCAMG 118


RESULT 5
LV6C_HUMAN
ID   LV6C_HUMAN     STANDARD;      PRT;   111 AA.
AC   P06317;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region SUT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
```

```
RN   [1]
RP   SEQUENCE.
RA   Solomon A., Kyle R.A., Frangione B.;
RT   "Light chain variable region subgroups of monoclonal immunoglobulins
RT   in amyloidosis AL.";
RL   (In) Glenner G.G., Osserman E.F., Benditt E.P., Calkins E.,
RL   Cohen A.S., Zucker-Franklin D. (eds.);
RL   Amyloidosis, pp.449-462, Plenum Press, New York (1986).
DR   PIR; A01988; L6HUST.
DR   PDB; 1CD0; 06-MAR-00.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; 3D-structure.
FT   DOMAIN        1     22       FRAMEWORK-1.
FT   DOMAIN       23     35       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       36     50       FRAMEWORK-2.
FT   DOMAIN       51     57       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       58     91       FRAMEWORK-3.
FT   DOMAIN       92    100       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      101    111       FRAMEWORK-4.
FT   DISULFID     22     91       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12247 MW;  0941DD547D983598 CRC64;

  Query Match             37.2%;  Score 200;  DB 1;  Length 111;
  Best Local Similarity   48.8%;  Pred. No. 3.6e-15;
  Matches   41;  Conservative   12;  Mismatches   25;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :||| |    ||  | | ||||| | ||  :::    ||  ||: :||||| :
Db         14 PGKTVIISCTRSDG--TIAGYYVQWYQQRPGRAPTTVIF----EDTQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :| ||:|||||
Db         68 DRSSNSASLTISGLQTEDEADYYC 91


RESULT 6
LV6A_HUMAN
ID   LV6A_HUMAN     STANDARD;      PRT;   112 AA.
AC   P01721;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-VI region AR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE (AMYLOID PROTEIN AR).
RX   MEDLINE=82091000; PubMed=6797401;
RA   Sletten K., Natvig J.B., Husby G., Juul J.;
RT   "The complete amino acid sequence of a prototype
RT   immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";
RL   Biochem. J. 195:561-572(1981).
CC   -!- MISCELLANEOUS: ABOUT HALF OF THE LAMBDA CHAIN C REGION IS MISSING
CC       FROM THIS PROTEIN.
CC   -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE SPLEEN OF A
CC       PATIENT WITH AMYLOIDOSIS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01987; L6HUAR.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1    107       IG-LIKE.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11918 MW;  570BCD9A368EF1FE CRC64;

  Query Match             36.6%;  Score 197;  DB 1;  Length 112;
  Best Local Similarity   47.6%;  Pred. No. 7.7e-15;
  Matches   40;  Conservative   15;  Mismatches   23;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:    ||| |    :| |  | ||||| |||| ::|    :|: ||: :||||| :
Db         14 PGKTVTFSCTGSGG--SIADSFVQWYQQRPGSAPTTVIY----DDNQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              |:: |:  |||| :: ||:|||||
Db         68 DDSANSASLTISGLKTEDEADYYC 91


RESULT 7
LV2F_HUMAN
ID   LV2F_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01709;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region MGC.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75013804; PubMed=4415202;
RA   Fett J.W., Deutsch H.F.;
RT   "Primary structure of the Mcg lambda chain.";
RL   Biochemistry 13:4102-4114(1974).
RN   [2]
RP   LAMBDA CHAIN GENES.
RX   MEDLINE=76093781; PubMed=812801;
RA   Fett J.W., Deutsch H.F.;
RT   "A new lambda-chain gene.";
RL   Immunochemistry 12:643-652(1975).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA   Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
RA   Panagiotopoulos N.;
RT   "Rotational allomerism and divergent evolution of domains in
RT   immunoglobulin light chains.";
RL   Biochemistry 14:3953-3961(1975).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=90133913; PubMed=2515285;
RA   Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
RT   "Three-dimensional structure of a light chain dimer crystallized in
RT   water. Conformational flexibility of a molecule in two crystal
RT   forms.";
RL   J. Mol. Biol. 210:601-615(1989).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH
CC       A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,
CC       SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A90381; L2HUMC.
DR   PDB; 2MCG; 15-JUL-92.
DR   PDB; 1A8J; 17-JUN-98.
DR   PDB; 1DCL; 15-MAY-97.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
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DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    108       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   STRAND        5      5
FT   STRAND       10     12
FT   STRAND       18     23
FT   TURN         26     32
FT   STRAND       36     40
FT   TURN         42     43
FT   STRAND       50     51
FT   TURN         52     54
FT   STRAND       55     55
FT   TURN         62     63
FT   STRAND       66     68
FT   STRAND       72     77
FT   HELIX        82     84
FT   STRAND       86     93
FT   STRAND       99    101
FT   STRAND      105    109
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11558 MW;  7CC1D6E2FA3377BA CRC64;

  Query Match             34.5%;  Score 185.5;  DB 1;  Length 111;
  Best Local Similarity   47.6%;  Pred. No. 1.4e-13;
  Matches   40;  Conservative   14;  Mismatches   23;  Indels    7;  Gaps    3;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              ||   :||| :   |   :| |||||| || ||: ::|    | : ||: :||||| :|
Db         15 GQSVTISCTGTSSDVGGYNY-VSWYQQHAGKAPKVIIY----EVNKRPSGVPDRFSGSK- 68

Qy         69 EAHNACVLTISPVQPEDDADYYCS 92
                : |   ||:| :| ||:||||||
Db         69 -SGNTASLTVSGLQAEDEADYYCS 91


RESULT 8
LV6D_HUMAN
ID   LV6D_HUMAN     STANDARD;      PRT;   111 AA.
AC   P06318;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region WLT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86122667; PubMed=4089539;
RA   Dwulet F.E., Strako K., Benson M.D.;
RT   "Amino acid sequence of a lambda VI primary (AL) amyloid protein
RT   (WLT).";
RL   Scand. J. Immunol. 22:653-660(1985).
DR   PIR; A01989; L6HULT.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     22       FRAMEWORK-1.
FT   DOMAIN       23     35       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       36     50       FRAMEWORK-2.
FT   DOMAIN       51     57       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       58     91       FRAMEWORK-3.
FT   DOMAIN       92    101       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      102    111       FRAMEWORK-4.
FT   DISULFID     22     91       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11966 MW;  0C88B2FE37BCE24F CRC64;

  Query Match             34.4%;  Score 185;  DB 1;  Length 111;
  Best Local Similarity   45.2%;  Pred. No. 1.6e-13;
  Matches   38;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              | :   :||| |   :|    | ||||| |||| ::|    |:: ||:::||||| :
Db         14 PEKTVTISCTGSSG--SIGSNYVQWYQQRPGSAPTNVIY----ENNQRPSEVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :: ||:|||||
Db         68 DSSSNSASLTISGLKTEDEADYYC 91


RESULT 9
LV6E_HUMAN
ID   LV6E_HUMAN     STANDARD;      PRT;   131 AA.
AC   P06319;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig lambda chain V-VI region EB4 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85215660; PubMed=3923440;
RA   Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT   "Cloning and sequence analysis of an Ig lambda light chain mRNA
RT   expressed in the Burkitt's lymphoma cell line EB4.";
RL   Nucleic Acids Res. 13:2931-2941(1985).
DR   PIR; A01990; L6HUEB.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    131       IG LAMBDA CHAIN V-VI REGION EB4.
FT   DOMAIN       20     41       FRAMEWORK-1.
FT   DOMAIN       42     54       COMPLEMENTARITY-DETERMINING-1.
FT   DOMAIN       55     69       FRAMEWORK-2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING-2.
FT   DOMAIN       77    110       FRAMEWORK-3.
FT   DOMAIN      111    118       COMPLEMENTARITY-DETERMINING-3.
FT   DOMAIN      119    131       FRAMEWORK-4.
FT   DISULFID     41    110       BY SIMILARITY.
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  14147 MW;  02A9179C8C05C2CD CRC64;

  Query Match             34.0%;  Score 183;  DB 1;  Length 131;
  Best Local Similarity   45.2%;  Pred. No. 3.2e-13;
  Matches   38;  Conservative   13;  Mismatches   27;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :|||      :|    | ||||| |||  ::|    ||: ||  :||||| :
Db         33 PGKTVTISCT--GNSGSIASNYVQWYQQRRVSAPTIVIY----EDNQRPLGVPDRFSGSI 86
```

```
Qy          68 DEAHNACVLTISPVQPEDDADYYC 91
                  | : |:  |||| :: ||:|||||
Db          87 DSSSNSASLTISGLKTEDEADYYC 110


RESULT 10
LV2L_HUMAN
ID   LV2L_HUMAN     STANDARD;      PRT;   111 AA.
AC   P80422;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig gamma lambda chain V-II region DOT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95255298; PubMed=7737190;
RA   Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT   "Characterization of the two unique human anti-flavin monoclonal
RT   immunoglobulins.";
RL   Eur. J. Biochem. 228:886-893(1995).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1    106       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11787 MW;  F358B1EA2CD7109A CRC64;

  Query Match             33.9%;  Score 182.5;  DB 1;  Length 111;
  Best Local Similarity   47.6%;  Pred. No. 3e-13;
  Matches   40;  Conservative   12;  Mismatches   25;  Indels    7;  Gaps    3;

Qy           8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
               |||   :||| |  |   |  |||||| | ||| |:|    :|  ||: :|:||| :|
Db          14 PGQAVTISCTGLPS-VVDDDNFVSWYQQTPGRAPRLLIY----DDSLRPSGVPNRFSGSK 68

Qy          68 DEAHNACVLTISPVQPEDDADYYC 91
                 :  |  |||| :||:|:| |:|
Db          69 SDTKAA--LTISGLQPDDEATYFC 90


RESULT 11
LV2G_HUMAN
ID   LV2G_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01710;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region BO.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71103825; PubMed=5532228;
RA   Wikler M., Putnam F.W.;
RT   "Amino acid sequence of human lambda chains. 3. Tryptic peptides,
RT   chymotryptic peptides, and sequence of protein Bo.";
RL   J. Biol. Chem. 245:4488-4507(1970).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01976; L2HUBO.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11785 MW;  92F5A1BF72421BAC CRC64;

  Query Match             33.6%;  Score 180.5;  DB 1;  Length 111;
  Best Local Similarity   44.7%;  Pred. No. 5e-13;
  Matches   38;  Conservative   14;  Mismatches   26;  Indels    7;  Gaps    3;

Qy           8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
               |||   :||| :   |    | ||||||  | ||: :::    |   ||: :|||||:|
Db          14 PGQSVTISCTGTSSDVGDNKY-VSWYQQHPGRAPKLVIF----EVSQRPSGVPDRFSGSK 68

Qy          68 DEAHNACVLTISPVQPEDDADYYCS 92
                 :  |   ||:| :: ||:||||||
Db          69 SD--NTASLTVSGLRAEDEADYYCS 91


RESULT 12
LV2K_HUMAN
ID   LV2K_HUMAN     STANDARD;      PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN
CC       INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Amyloid; Bence-Jones protein.
FT   DOMAIN        1    102       IG-LIKE.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11581 MW;  988FEF363AE1E4F3 CRC64;

  Query Match             32.6%;  Score 175.5;  DB 1;  Length 112;
  Best Local Similarity   47.1%;  Pred. No. 1.8e-12;
  Matches   40;  Conservative   13;  Mismatches   25;  Indels    7;  Gaps    3;
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Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   |: |||||  | ||: |:|    : : ||: | :||| :|
Db         14 PGQSITISCTGTTSDVGGYDF-VSWYQQHPGKAPKLLIY----DVNSRPSGISNRFSGSK 68

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   |||| :| ||:||||||
Db         69 --SGNTASLTISGLQAEDEADYYCS 91


RESULT 13
LV2I_HUMAN
ID   LV2I_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01712;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region WIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=79062503; PubMed=102365;
RA   Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT   "Amino acid sequence of the human myeloma lambda chain Win.";
RL   Biochim. Biophys. Acta 537:9-21(1978).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01978; L2HUWN.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11694 MW;  8C3CE95FE721B87C CRC64;

  Query Match             32.5%;  Score 175;  DB 1;  Length 111;
  Best Local Similarity   44.9%;  Pred. No. 2e-12;
  Matches   40;  Conservative   15;  Mismatches   26;  Indels    8;  Gaps    4;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| |  :||  :: ||||||   |  |: ::|    :   ||: :|||||  :|
Db         14 PGQSVTISCTGSYSNVTGYNH-VSWYQQDPGKVPKLMIY----DVDKRPSGVPDRFSGSK 68

Qy         68 DEAHNACVLTISPVQPEDDADYYCSVGYG 96
                : |   |||| :|  ::||||||  ||
Db         69 --SANTASLTISGLQANNEADYYCS-SYG 94


RESULT 14
LV2E_HUMAN
ID   LV2E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01708;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-II region BUR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80006606; PubMed=113407;
RA   Infante A.J., Putnam F.W.;
RT   "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
RT   sequence of a human IgA lambda light chain (Bur).";
RL   J. Biol. Chem. 254:9006-9016(1979).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
CC       MARKERS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01974; L2HUBR.
DR   HSSP; P01709; 2MCG.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       IG-LIKE.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     22     90       BY SIMILARITY.
FT   SITE         91     91       APPEARS TO BE A FREE BUT UNREACTIVE
FT                                SULFHYDRYL GROUP.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11506 MW;  BFD8AE1C5D267FAB CRC64;

  Query Match             32.1%;  Score 172.5;  DB 1;  Length 109;
  Best Local Similarity   45.2%;  Pred. No. 3.7e-12;
  Matches   38;  Conservative   12;  Mismatches   27;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||    :||  :  :|    | ||||||  | ||: ::|    |   ||: :|||||  :|
Db         14 PGHSVTISCIGTSSNVGDYKY-VSWYQQHPGKAPKLIIY----EVSSRPSGVPDRFSGSK 68

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
                : |   |||| :| ||:|||||
Db         69 --SGNTASLTISGLQAEDEADYYC 90


RESULT 15
LV3A_HUMAN
ID   LV3A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01714;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ig lambda chain V-III region SH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70166723; PubMed=4909564;
RA   Titani K., Wikler M., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a lambda type Bence-Jones protein. 3. The
RT   complete amino acid sequence and the location of the disulfide
RT   bridges.";
RL   J. Biol. Chem. 245:2171-2176(1970).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR   PIR; A01980; L3HUSH.
DR   HSSP; P80748; 2LOI.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     97       IG-LIKE.
FT   DISULFID     21     86
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11392 MW;  E7E1229586411A56 CRC64;

  Query Match             31.8%;  Score 171;  DB 1;  Length 108;
  Best Local Similarity   42.2%;  Pred. No. 5.4e-12;
  Matches   38;  Conservative   17;  Mismatches   25;  Indels   10;  Gaps    4;

Qy          3 ALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDR 62
              |: |  ||  :::|    |  ::| |  :||||: | ||  ::| |    ::||: ||||
Db          8 AVSVALGQTVRITC----QGDSLRGYDAAWYQQKPGQAPLLVIYGR----NNRPSGIPDR 59

Qy         63 FSAAKDEAHNACVLTISPVQPEDDADYYCS 92
              || :    | |  |||:  | ||:|||||:
Db         60 FSGS-SSGHTAS-LTITGAQAEDEADYYCN 87


Search completed: June 28, 2004, 08:29:17
Job time : 9.91892 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:34 ; Search time 32.5541 Seconds
(without alignments)
959.521 Million cell updates/sec

Title: US-09-981-876-200_COPY_25_123
Perfect score: 538
Sequence: 1 LDALLVFPGQVAQLSCTLSP.....PVQPEDDADYYCSVGYGFSP 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	372.5	69.2	123	11	Q61243	Q61243 mus musculu
2	215.5	40.1	230	4	Q7Z2U3	Q7z2u3 homo sapien
3	199	37.0	135	4	Q9H5Z4	Q9h5z4 homo sapien
4	197	36.6	112	4	Q96JD1	Q96jd1 homo sapien
5	193	35.9	112	4	Q96JD2	Q96jd2 homo sapien
6	189.5	35.2	116	4	Q96JD0	Q96jd0 homo sapien
7	175	32.5	237	4	Q8WTU6	Q8wtu6 homo sapien
8	174.5	32.4	236	4	Q96E61	Q96e61 homo sapien
9	172.5	32.1	237	4	Q8WUK4	Q8wuk4 homo sapien
10	172.5	32.1	240	4	Q8WUK3	Q8wuk3 homo sapien
11	169	31.4	107	4	Q9NSD6	Q9nsd6 homo sapien
12	166	30.9	109	4	Q9UL86	Q9ul86 homo sapien
13	165	30.7	233	4	Q8TBC9	Q8tbc9 homo sapien
14	161	29.9	234	4	Q8N355	Q8n355 homo sapien
15	161	29.9	235	11	Q99M11	Q99m11 mus musculu
16	160	29.7	108	4	Q96SB0	Q96sb0 homo sapien
17	158	29.4	109	4	Q9UL78	Q9ul78 homo sapien
18	158	29.4	236	4	Q8NEJ1	Q8nej1 homo sapien
19	157	29.2	110	4	Q8TE63	Q8te63 homo sapien
20	156	29.0	81	4	Q7Z2E8	Q7z2e8 homo sapien
21	155	28.8	233	4	Q96I69	Q96i69 homo sapien
22	153	28.4	234	4	Q7Z2U7	Q7z2u7 homo sapien
23	151.5	28.2	100	6	O77624	O77624 bos taurus
24	151	28.1	101	4	Q8IZD8	Q8izd8 homo sapien
25	151	28.1	233	4	Q8N5F4	Q8n5f4 homo sapien
26	150.5	28.0	105	4	Q8WVJ6	Q8wvj6 homo sapien
27	148	27.5	107	4	Q9UL82	Q9ul82 homo sapien
28	138	25.7	132	4	Q8TBD0	Q8tbd0 homo sapien
29	137	25.5	108	4	Q9UL83	Q9ul83 homo sapien
30	134	24.9	97	4	O43234	O43234 homo sapien
31	134	24.9	107	11	Q9ERZ9	Q9erz9 mus musculu
32	133.5	24.8	484	11	Q8VEA0	Q8vea0 mus musculu
33	132	24.5	109	4	Q9UL85	Q9ul85 homo sapien
34	130.5	24.3	99	11	Q9JL74	Q9jl74 mus musculu
35	129	24.0	111	11	Q811U6	Q811u6 mus musculu
36	128	23.8	107	4	Q96SA9	Q96sa9 homo sapien
37	128	23.8	108	4	Q9UL77	Q9ul77 homo sapien
38	127.5	23.7	239	4	Q8NEK0	Q8nek0 homo sapien
39	127	23.6	108	4	Q9UL79	Q9ul79 homo sapien
40	127	23.6	248	13	Q7SYU1	Q7syu1 xenopus lae
41	126	23.4	236	11	Q7TMK3	Q7tmk3 mus musculu
42	125	23.2	237	13	Q7SZ36	Q7sz36 xenopus lae
43	124.5	23.1	114	4	Q9UL80	Q9ul80 homo sapien
44	124	23.0	131	11	Q811C3	Q811c3 mus musculu
45	124	23.0	494	4	Q96K68	Q96k68 homo sapien

ALIGNMENTS

RESULT 1
Q61243
ID Q61243 PRELIMINARY; PRT; 123 AA.
AC Q61243;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 8HS20 protein precursor (Pre-B lymphocyte gene 3).
GN VPREB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=93259124; PubMed=8491176;
RA Shirasawa T., Ohnishi K., Hagiwara S., Shigemoto K., Takebe Y.,
RA Rajewsky K., Takemori T.;
RT "A novel gene product associated with mu chains in immature B cells.";
RL EMBO J. 12:1827-1834(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

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RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; D13208; BAA02495.1; -.
DR   EMBL; AK008794; BAB25899.1; -.
DR   PIR; S35302; S35302.
DR   HSSP; P01709; 2MCG.
DR   MGD; MGI:98938; Vpreb3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   CHAIN        20    123       8HS20 PROTEIN.
SQ   SEQUENCE   123 AA;  13400 MW;  2A1AD371D1CEE98F CRC64;

  Query Match             69.2%;  Score 372.5;  DB 11;  Length 123;
  Best Local Similarity   69.4%;  Pred. No. 6.5e-35;
  Matches   68;  Conservative   11;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          2 DALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPD 61
              ||  ||||| | ||||:: || |  | |||||||: |||| :|||| :||:|:|||||||
Db         27 DAFSVFPGQDAHLSCTINSQHATAGDIGVSWYQQQPGSAP-HLLYYYAEEEHYRPADIPD 85

Qy         62 RFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              ||||  | |||||:|||||| |||||||:||: : | |
Db         86 RFSATVDAAHNACILTISPVLPEDDADYFCSIAHTFEP 123


RESULT 2
Q7Z2U3
ID   Q7Z2U3      PRELIMINARY;      PRT;   230 AA.
AC   Q7Z2U3;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054893; AAH54893.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   230 AA;  24853 MW;  8BE60CC824BB886E CRC64;

  Query Match             40.1%;  Score 215.5;  DB 4;  Length 230;
  Best Local Similarity   45.1%;  Pred. No. 1.4e-16;
  Matches   41;  Conservative   20;  Mismatches   29;  Indels    1;  Gaps    1;

Qy          3 ALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDR 62
              :|   ||  | |:|||  :   : || : ||||::| :|:||| :||: |  : : :| |
Db         18 SLSASPGASASLTCTLR-RGFYVVDYRIYWYQQKSGRSPQYLLRHRSDSDKQQGSGVPSR 76

Qy         63 FSAAKDEAHNACVLTISPVQPEDDADYYCSV 93
              || :|| : || :| || :: ||:|||||
Db         77 FSGSKDASANAGILVISGLRSEDEADYYCMV 107


RESULT 3
Q9H5Z4
ID   Q9H5Z4      PRELIMINARY;      PRT;   135 AA.
AC   Q9H5Z4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ22755.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ileal mucosa;
RA   Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
RA   Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
RA   Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
RA   Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
RA   Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK026408; BAB15473.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   135 AA;  14780 MW;  652492DED930F401 CRC64;

  Query Match             37.0%;  Score 199;  DB 4;  Length 135;
  Best Local Similarity   45.3%;  Pred. No. 5.9e-15;
  Matches   34;  Conservative   17;  Mismatches   24;  Indels    0;  Gaps    0;

Qy         24 TIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTISPVQP 83
              :: |: : ||||: |: ||||||| |: :  : : :| ||| : | : || :| || :||
Db          7 SVGDFWIRWYQQKPGNPPRYLLYYHSDSNKGQGSGVPSRFSGSNDASANAGILRISGLQP 66

Qy         84 EDDADYYCSVGYGFS 98
              ||:|||||   :  |
Db         67 EDEADYYCGTWHSNS 81


RESULT 4
Q96JD1
ID   Q96JD1      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region PIP (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
```

```
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region PIP.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267874; AAK58586.1; -.
DR   PIR; A30323; A30323.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12047 MW;  0D3885AC23567B9F CRC64;

  Query Match             36.6%;  Score 197;  DB 4;  Length 112;
  Best Local Similarity   47.6%;  Pred. No. 8e-15;
  Matches   40;  Conservative   14;  Mismatches   24;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :||| |    :|    | ||||| |||| ::|    ||: ||: :||||| :
Db         14 PGKTITISCTRSSG--SIASNYVQWYQQRPGSAPTTVIY----EDNQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :: ||:|||||
Db         68 DSSSNSASLTISGLKTEDEADYYC 91


RESULT 5
Q96JD2
ID   Q96JD2      PRELIMINARY;      PRT;   112 AA.
AC   Q96JD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region NEG (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region NEG.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267873; AAK58585.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11908 MW;  080B4B37E2360B06 CRC64;

  Query Match             35.9%;  Score 193;  DB 4;  Length 112;
  Best Local Similarity   46.4%;  Pred. No. 2.3e-14;
  Matches   39;  Conservative   13;  Mismatches   26;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :||| |     |    | ||||| |||| ::|    |:: ||: :||||| :
Db         14 PGKTITISCTGSSGR--IASNSVQWYQQRPGSAPNIVMY----ENNQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :  ||:|||||
Db         68 DSSSNSASLTISGLMTEDEADYYC 91


RESULT 6
Q96JD0
ID   Q96JD0      PRELIMINARY;      PRT;   116 AA.
AC   Q96JD0;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Amyloid lambda 6 light chain variable region SAR (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RA   Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT   "Amyloid lambda 6 light chain variable region SAR.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF267875; AAK58587.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12294 MW;  F7B0E9F49FAE369E CRC64;

  Query Match             35.2%;  Score 189.5;  DB 4;  Length 116;
  Best Local Similarity   44.6%;  Pred. No. 6e-14;
  Matches   41;  Conservative   16;  Mismatches   24;  Indels   11;  Gaps    4;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :||| |    :   :| | ||| | |||| ::|    ||: ||: :|||||
Db         14 PGKTVTISCTGSSGSIA-TNY-VQWYQLRPGSAPTTVIY----EDNQRPSGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC-----SVG 94
              | : |:  |||| :: ||:|||||     |:|
Db         68 DSSSNSASLTISGLKTEDEADYYCQSYDSSIG 99


RESULT 7
Q8WTU6
ID   Q8WTU6      PRELIMINARY;      PRT;   237 AA.
AC   Q8WTU6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022098; AAH22098.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24884 MW;  E6CF371E753968E8 CRC64;

  Query Match             32.5%;  Score 175;  DB 4;  Length 237;
  Best Local Similarity   42.9%;  Pred. No. 6.5e-12;
  Matches   39;  Conservative   16;  Mismatches   28;  Indels    8;  Gaps    4;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| |  ::    | | ||||  |:||: |:|  |    :||: :||||| :|
Db         33 PGQRVTISCTGSSSNIG-AGYDVHWYQQLPGTAPKLLIYGNS----NRPSGVPDRFSGSK 87
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Qy          68 DEAHNACVLTISPVQPEDDADYYCSVGYGFS 98
                  :  :  | |: :| ||:|||||   | :|
Db          88 --SGTSASLAITGLQAEDEADYYCQ-SYDYS 115


RESULT 8
Q96E61
ID   Q96E61      PRELIMINARY;      PRT;   236 AA.
AC   Q96E61;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC012876; AAH12876.1; -.
DR   PIR; S12440; S12440.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  24712 MW;  7EC9FB3622FED957 CRC64;

  Query Match           32.4%;  Score 174.5;  DB 4;  Length 236;
  Best Local Similarity  42.9%;  Pred. No. 7.3e-12;
  Matches   36;  Conservative   17;  Mismatches   24;  Indels    7;  Gaps    3;

Qy           8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
               |||   :||| |  ::    | | |||| |:||: |:|     :::||: :||||| :|
Db          33 PGQTVTISCTGSSTNIG-AGYAVHWYQQFPGAAPKVLIY----GNYNRPSGVPDRFSGSK 87

Qy          68 DEAHNACVLTISPVQPEDDADYYC 91
                  :  :  | |: :| ||:|||||
Db          88 --SGTSASLAITGLQAEDEADYYC 109


RESULT 9
Q8WUK4
ID   Q8WUK4      PRELIMINARY;      PRT;   237 AA.
AC   Q8WUK4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020233; AAH20233.1; -.
DR   PIR; S12441; S12441.
DR   PIR; S12627; S12627.
DR   PIR; S29258; S29258.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   237 AA;  24897 MW;  73C7D70B8039D186 CRC64;

  Query Match           32.1%;  Score 172.5;  DB 4;  Length 237;
  Best Local Similarity  44.0%;  Pred. No. 1.3e-11;
  Matches   37;  Conservative   15;  Mismatches   25;  Indels    7;  Gaps    3;

Qy           8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
               |||   :||| |  ::    | | |||| |:||: |:|  |    :||: :||||| :|
Db          33 PGQRVTISCTGSSSNIG-AGYDVHWYQQLPGTAPKLLIYGNS----NRPSGVPDRFSGSK 87

Qy          68 DEAHNACVLTISPVQPEDDADYYC 91
                  :  :  | |: :| ||:|||||
Db          88 --SGTSASLAITGLQAEDEADYYC 109


RESULT 10
Q8WUK3
ID   Q8WUK3      PRELIMINARY;      PRT;   240 AA.
AC   Q8WUK3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tonsil;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC020236; AAH20236.1; -.
DR   PIR; S16439; S16439.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   240 AA;  25977 MW;  921E47DDCA7259F0 CRC64;

  Query Match           32.1%;  Score 172.5;  DB 4;  Length 240;
  Best Local Similarity  36.4%;  Pred. No. 1.3e-11;
  Matches   36;  Conservative   20;  Mismatches   30;  Indels   13;  Gaps    3;

Qy           7 FPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAA 66
               | |   :|:|||| :|     | : ||||| | :|:|::  :|:  |::  ||||| :
Db          32 FLGASIKLTCTLSREH---SSYTIEWYQQRPGRSPQYIMKVKSDGSHNKGDGIPDRFMGS 88

Qy          67 KDEAHNACVLTISPVQPEDDADYYC--------SVGYGF 97
                     ||:| :| :|:|:|:|          ||: |
Db          89 SSGADR--YLTLSNLQSDDEAEYHCGESHTIDGQVGWVF 125


RESULT 11
Q9NSD6
ID   Q9NSD6      PRELIMINARY;      PRT;   107 AA.
AC   Q9NSD6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymphocytes;
RA   Hohmann A.;
RT   "Autoimmunity.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L43092; AAA69746.2; -.
DR   HSSP; P01709; 2MCG.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11306 MW;  A2B04B37187A5F00 CRC64;

  Query Match             31.4%;  Score 169;  DB 4;  Length 107;
  Best Local Similarity   41.7%;  Pred. No. 1.2e-11;
  Matches   35;  Conservative   17;  Mismatches   22;  Indels   10;  Gaps    3;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              ||  :::|    |  ::| |  |||||: | ||  ::| :    ::||: |||||| :
Db         13 GQTVRITC----QGDSLRSYYASWYQQKPGQAPVLVIYGK----NNRPSGIPDRFSGS-- 62

Qy         69 EAHNACVLTISPVQPEDDADYYCS 92
              : |   |||:   | ||:|||||:
Db         63 SSGNTASLTITGAQAEDEADYYCN 86


RESULT 12
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -.
DR   PIR; B30607; B30607.
DR   PIR; I30601; I30601.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

  Query Match             30.9%;  Score 166;  DB 4;  Length 109;
  Best Local Similarity   44.2%;  Pred. No. 2.8e-11;
  Matches   42;  Conservative   11;  Mismatches   32;  Indels   10;  Gaps    4;

Qy          4 LLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRF 63
              | :|||: | |||  |    ::    ::||||: | ||| |:|  |     |   |||||
Db         11 LSLFPGERATLSCRASQ---SVSSSYLAWYQQKPGQAPRLLIYGTSS----RATGIPDRF 63

Qy         64 SAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFS 98
              | :  |      |||| ::||| | |||   || |
Db         64 SGSGSETD--FTLTISRLEPEDFAVYYCQ-QYGSS 95


RESULT 13
Q8TBC9
ID   Q8TBC9      PRELIMINARY;      PRT;   233 AA.
AC   Q8TBC9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=B-cell;
RA   Strausberg R.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC022823; AAH22823.1; -.
DR   PIR; S12442; S12442.
DR   PIR; S30526; S30526.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   233 AA;  24867 MW;  367411BFD6F4DF92 CRC64;

  Query Match             30.7%;  Score 165;  DB 4;  Length 233;
  Best Local Similarity   41.6%;  Pred. No. 8.9e-11;
  Matches   37;  Conservative   15;  Mismatches   21;  Indels   16;  Gaps    4;

Qy          6 VFPGQVAQLSCT---LSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDR 62
              | |||  |:::|:   |  |:          ||||: | ||  ::|    :|: ||: ||:|
Db         31 VSPGQTARITCSGDALPKQY-------AYWYQQKPGQAPVLVIY----KDNERPSGIPER 79

Qy         63 FSAAKDEAHNACVLTISPVQPEDDADYYC 91
              || :   :     |||| || ||:|||||
Db         80 FSGS--SSGTTVTLTISGVQAEDEADYYC 106


RESULT 14
Q8N355
ID   Q8N355      PRELIMINARY;      PRT;   234 AA.
AC   Q8N355;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC028090; AAH28090.1; -.
DR   PIR; S12441; S12441.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
```

```
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   234 AA;  24792 MW;  CC848CAEBA4A9D63 CRC64;

  Query Match             29.9%;  Score 161;  DB 4;  Length 234;
  Best Local Similarity   40.9%;  Pred. No. 2.6e-10;
  Matches   36;  Conservative   14;  Mismatches   28;  Indels   10;  Gaps    3;

Qy          6 VFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
              | ||| |:::|  :     |    | ||||: | ||  ::|    :|  ||: ||:|||
Db         31 VAPGQTARITCGGN----NIGSKSVHWYQQKPGQAPVLVVY----DDSDRPSGIPERFSG 82

Qy         66 AKDEAHNACVLTISPVQPEDDADYYCSV 93
              :  : |   |||| |   |:|||| :
Db         83 S--NSGNTATLTISRVDAGDEADYYCQL 108


RESULT 15
Q99M11
ID   Q99M11      PRELIMINARY;      PRT;   235 AA.
AC   Q99M11;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002129; AAH02129.1; -.
DR   HSSP; P01703; 7FAB.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   235 AA;  25403 MW;  39807BFE6782A3FB CRC64;

  Query Match             29.9%;  Score 161;  DB 11;  Length 235;
  Best Local Similarity   42.2%;  Pred. No. 2.6e-10;
  Matches   35;  Conservative   13;  Mismatches   29;  Indels    6;  Gaps    2;

Qy          9 GQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKD 68
              |  |:| |  |  :  | |  |:||||  | :|  ::|     |  ||: : |||| : |
Db         34 GSTAKLPCKASTGN--IGDSYVNWYQQYMGRSPTNMIY----GDDLRPSGVSDRFSGSID 87

Qy         69 EAHNACVLTISPVQPEDDADYYC 91
              : |:  |||  || :|:|||||
Db         88 SSSNSAFLTIQNVQADDEADYYC 110


Search completed: June 28, 2004, 08:27:58
Job time : 32.5541 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 28, 2004, 08:24:34 ; Search time 45.4865 Seconds
(without alignments)
614.956 Million cell updates/sec

Title: US-09-981-876-200_COPY_25_123
Perfect score: 538
Sequence: 1 LDALLVFPGQVAQLSCTLSP.....PVQPEDDADYYCSVGYGFSP 99

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	538	100.0	113	4	AAM41476	Aam41476 Human pol
2	538	100.0	123	2	AAW75123	Aaw75123 Human sec
3	538	100.0	123	3	AAY66655	Aay66655 Membrane-
4	538	100.0	123	3	AAB24061	Aab24061 Human PRO
5	538	100.0	123	4	AAU12372	Aau12372 Human PRO
6	538	100.0	123	4	AAB65178	Aab65178 Human PRO
7	538	100.0	123	6	ABU57993	Abu57993 Human PRO
8	538	100.0	123	6	ABU59071	Abu59071 Novel hum
9	538	100.0	123	6	ABU82583	Abu82583 Human sec
10	538	100.0	123	6	ABO17816	Abo17816 Novel hum
11	538	100.0	123	6	ABU60502	Abu60502 Human sec
12	538	100.0	123	6	ABU13884	Abu13884 Human PRO
13	538	100.0	123	6	ABU81070	Abu81070 Human PRO
14	538	100.0	123	6	ABU72469	Abu72469 Novel hum
15	538	100.0	123	6	ABU66770	Abu66770 Human PRO
16	538	100.0	123	6	ABU59851	Abu59851 Novel sec
17	538	100.0	123	6	ABU59218	Abu59218 Human sec
18	538	100.0	123	6	ABO25915	Abo25915 Human PRO
19	538	100.0	123	6	ABO25041	Abo25041 Human sec
20	538	100.0	123	6	ABO01999	Abo01999 Novel hum
21	538	100.0	123	6	ABU58924	Abu58924 Human sec
22	538	100.0	123	6	ABU92302	Abu92302 Novel hum
23	538	100.0	123	6	ABU59367	Abu59367 Novel hum
24	538	100.0	123	6	ABU67046	Abu67046 Human sec
25	538	100.0	123	6	ABU92133	Abu92133 Novel hum
26	538	100.0	123	6	ABU10839	Abu10839 Human PRO
27	538	100.0	123	6	ABU81591	Abu81591 Novel hum
28	538	100.0	123	6	ABU88530	Abu88530 Human sec
29	538	100.0	123	6	ABO34044	Abo34044 Human PRO
30	538	100.0	123	6	ADA45921	Ada45921 Novel hum
31	538	100.0	123	6	ADA76352	Ada76352 Human PRO
32	538	100.0	123	6	ADA19002	Ada19002 Human PRO
33	538	100.0	123	6	ADA61625	Ada61625 Homo sapi
34	538	100.0	123	6	ADB19410	Adb19410 Novel hum
35	538	100.0	123	6	ADB27951	Adb27951 Human PRO
36	538	100.0	123	6	ADA86430	Ada86430 Novel hum
37	538	100.0	123	6	ADB15994	Adb15994 Human PRO
38	538	100.0	123	6	ADA37628	Ada37628 Human sec
39	538	100.0	123	6	ADA47780	Ada47780 Human PRO
40	538	100.0	123	6	ADA21314	Ada21314 Human sec
41	538	100.0	123	6	ADA10101	Ada10101 Human sec
42	538	100.0	123	6	ADA67575	Ada67575 Human PRO
43	538	100.0	123	6	ADB30582	Adb30582 Human PRO
44	538	100.0	123	6	ADA85878	Ada85878 Novel hum
45	538	100.0	123	6	ADA17645	Ada17645 Human PRO

ALIGNMENTS

RESULT 1
AAM41476
ID AAM41476 standard; protein; 113 AA.
XX
AC AAM41476;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 6407.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60632.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 6407; 10078pp; English.

XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 113 AA;

Query Match 100.0%; Score 538; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 9.1e-52;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         15 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 74

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         75 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 113
```

RESULT 2
AAW75123
ID AAW75123 standard; protein; 123 AA.
XX
AC AAW75123;
XX
DT 25-MAR-2003 (revised)
DT 28-JAN-1999 (first entry)
XX
DE Human secreted protein encoded by gene 67 clone HRGDF73.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839446-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US004482.
XX
PR 07-MAR-1997; 97US-0038621P.
PR 07-MAR-1997; 97US-0040161P.
PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.

PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057761P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
DR WPI; 1998-609887/51.
DR N-PSDB; AAV34220.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 320-321; 447pp; English.
XX
CC This sequence represents a secreted human protein encoded by the gene
CC clone detailed in the descriptor line. The gene can be used to generate
CC fusion proteins by linking to the gene to a human immunoglobulin Fc
CC portion (e.g. AAV34145) for increasing the stability of the fused protein
CC as compared to the human protein only. The invention relates to 70 novel
CC genes and their fragments (nucleic acid sequences: AAV34154-V34276; amino
CC acid sequences AAW75057-W75179) which are useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. Also,
CC pathological conditions can be diagnosed by determining the amount of the
CC new polypeptides in a sample or by determining the presence of mutations
CC in the new polynucleotides. Specific uses are described for each of the
CC 70 polynucleotides, based on which tissues they are most highly expressed
CC in (see AAV34154 for described uses). (Updated on 25-MAR-2003 to correct
CC PF field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 3
AAY66655
ID AAY66655 standard; protein; 123 AA.
XX
AC AAY66655;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO619.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN WO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088730P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088741P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089947P.
PR 19-JUN-1998; 98US-0089948P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 23-JUN-1998; 98US-0090349P.
PR 23-JUN-1998; 98US-0090355P.
PR 24-JUN-1998; 98US-0090429P.
PR 24-JUN-1998; 98US-0090431P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090445P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090472P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090538P.
PR 24-JUN-1998; 98US-0090540P.
PR 24-JUN-1998; 98US-0090557P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090691P.
PR 25-JUN-1998; 98US-0090694P.

PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 01-JUL-1998; 98US-0091358P.
PR 01-JUL-1998; 98US-0091360P.
PR 02-JUL-1998; 98US-0091478P.
PR 02-JUL-1998; 98US-0091486P.
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUL-1998; 98US-0091544P.
PR 02-JUL-1998; 98US-0091626P.
PR 02-JUL-1998; 98US-0091628P.
PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
PR 04-AUG-1998; 98US-0095318P.
PR 04-AUG-1998; 98US-0095321P.
PR 04-AUG-1998; 98US-0095325P.
PR 10-AUG-1998; 98US-0095916P.
PR 10-AUG-1998; 98US-0095929P.
PR 10-AUG-1998; 98US-0096012P.
PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
DR WPI; 2000-072883/06.
DR N-PSDB; AAZ64983.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX
PS Claim 12; Fig 68; 822pp; English.
XX
CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy 61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
|||||||||||||||||||||||||||||||||||||
Db 85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123

RESULT 4
AAB24061
ID AAB24061 standard; protein; 123 AA.
XX
AC AAB24061;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO619 protein sequence SEQ ID NO:16.
XX
KW Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
KW proliferation; tumourigenesis; identification; cancer; cytostatic;
KW nootropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
PN WO200053755-A2.
XX
PD 14-SEP-2000.
XX
PF 06-JAN-2000; 2000WO-US000376.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 30-NOV-1999; 99WO-US028313.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
PI Watanabe CK, Wood WI;
XX
DR WPI; 2000-572270/53.
DR N-PSDB; AAC58371.
XX
PT Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
PT treatment, diagnosis and prevention of cancer.
XX
PS Claim 61; Fig 10; 286pp; English.
XX
CC The present invention describes an isolated antibody that binds to one of
CC the human PRO proteins designated PRO212, PRO290, PRO341, PRO535, PRO619,
CC PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009, PRO1025,
CC PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184, PRO1187,
CC PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094, PRO2145 OR
CC PRO2198. PRO antagonists can be used to inhibit tumour cell growth. The
CC PRO polypeptides and nucleotides are useful in the treatment, diagnosis
CC and prevention of cancer. The antibodies and other anti-tumour compounds
CC maybe used to treat various conditions, including those characterised by
CC overexpression and/or activation of the amplified PRO genes. Exemplary
CC conditions or disorders to be treated with such antibodies and other
CC compounds include benign or malignant tumours (e.g., renal, liver,
CC kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas,
CC glioblastomas, and various head and neck tumours), leukaemias and
CC lymphoid malignancies, other disorders such as neuronal, glial,
CC astrocytal, hypothalamic and other glandular, macrophagal, epithelial,
CC stromal and blastocoelic disorders, and inflammatory, angiogenic and
CC immunologic disorders. AAC58242 to AAC58366 represent PCR primers and
CC hybridisation probes used in the isolation of the human PRO sequences.
CC AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human PRO
CC polynucleotide and protein sequences given in the exemplification of the
CC present invention
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 3; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
```

RESULT 5
AAU12372
ID AAU12372 standard; protein; 123 AA.
XX
AC AAU12372;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO619 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21444.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 402; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules

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CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 538;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
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Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 6
AAB65178
ID   AAB65178 standard; protein; 123 AA.
XX
AC   AAB65178;
XX
DT   02-APR-2001  (first entry)
XX
DE   Human PRO619 (UNQ355) protein sequence SEQ ID NO:117.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
KW   cancer; chromosomal mapping; gene mapping; tissue typing;
KW   diagnostic assay.
XX
OS   Homo sapiens.
XX
PN   WO200073454-A1.
XX
PD   07-DEC-2000.
XX
PF   30-MAR-2000; 2000WO-US008439.
XX
PR   02-JUN-1999;   99WO-US012252.
PR   23-JUN-1999;   99US-0141037P.
PR   07-JUL-1999;   99US-0143048P.
PR   20-JUL-1999;   99US-0144758P.
PR   26-JUL-1999;   99US-0145698P.
PR   28-JUL-1999;   99US-0146222P.
PR   17-AUG-1999;   99US-0149396P.
PR   15-SEP-1999;   99WO-US021090.
PR   15-SEP-1999;   99WO-US021547.
PR   08-OCT-1999;   99US-0158663P.
PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2001-032160/04.
DR   N-PSDB; AAF44129.
XX
PT   PRO polynucleotides used to produce polypeptides used to target bioactive
PT   molecules such as toxins, radiolabels or antibodies, to specific cells,
PT   to cause targeted cell death.
XX
PS   Claim 12; Fig 68; 935pp; English.
XX
CC   The present invention describes human secreted and transmembrane PRO
CC   proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC   be used for targeted delivery of bioactive molecules, such as toxins,
CC   radiolabels or antibodies, that cause cell death. PRO nucleotide
CC   sequences, and their fragments, can be used as hybridisation probes, in
CC   chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC   DNA. They may also be used to produce transgenic animals which are used
CC   to develop and screen therapeutically useful reagents. The PRO nucleotide
CC   and protein sequence can be used for tissue typing and in treating
CC   cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC   AAF44470 represent PCR primers and hybridisation probes used in the
CC   isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC   AAB65300 represent human PRO polynucleotide and protein sequences given
CC   in the exemplification of the present invention
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 538;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 7
ABU57993
ID   ABU57993 standard; protein; 123 AA.
XX
AC   ABU57993;
XX
DT   14-APR-2003  (first entry)
XX
DE   Human PRO polypeptide #25.
XX
KW   Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW   horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;
KW   antibody-dependent enzyme mediated prodrug therapy.
XX
OS   Homo sapiens.
XX
PN   US2003027163-A1.
XX
PD   06-FEB-2003.
XX
PF   15-NOV-2001; 2001US-00997666.
XX
PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
PR   05-NOV-1997;   97WO-US020069.
PR   12-NOV-1997;   97US-0065186P.
PR   13-NOV-1997;   97US-0065311P.
PR   24-NOV-1997;   97US-0066770P.
PR   25-FEB-1998;   98US-0075945P.
PR   20-MAR-1998;   98US-0078910P.
PR   28-APR-1998;   98US-0083322P.
PR   07-MAY-1998;   98US-0084600P.
PR   28-MAY-1998;   98US-0087106P.
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PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.
PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
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PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
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PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 8
ABU59071
ID ABU59071 standard; protein; 123 AA.
XX
AC ABU59071;
XX
DT 28-APR-2003 (first entry)
XX
DE Novel human secreted or transmembrane protein PRO619.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosum; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2002132252-A1.
XX
PD 19-SEP-2002.
XX
PF 14-NOV-2001; 2001US-00990442.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
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PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
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PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.

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PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   28-AUG-2001; 2001US-00941992.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-247083/24.
DR   N-PSDB; ABX80196.
XX
PT   Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT   and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT   are therapeutically useful for enhancing immune response and in cancer
PT   treatments.
XX
PS   Claim 12; Fig 68; 648pp; English.
XX
CC   The invention describes an isolated human PRO polypeptide. The PRO
CC   polypeptides are useful in detecting PRO polypeptides in a sample, in
CC   linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC   in modulating at least one biological activity of a cell expressing a PRO
CC   polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
CC   useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC   stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC   PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC   PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC   useful for treating conditions or disorders where angiogenesis would be
CC   beneficial, e.g. wound healing and antagonist of this polypeptide are
CC   useful for treating cancerous tumours. PRO812 inhibits vascular
CC   endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC   cells and is thus useful for inhibiting endothelial cell growth in
CC   mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC   PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC   stimulated T-lymphocytes and are therapeutically useful for enhancing
CC   immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC   retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC   rod photoreceptor cells) and therefore are useful for treating retinal
CC   disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC   and PRO11066 induce proliferation of mammalian kidney mesangial cells,
CC   and therefore are useful for treating kidney disorders associated with
CC   decreased mesangial cell function such as Berger disease or other
CC   nephropathies associated with dermatitis, herpetiformis or Crohn's
CC   disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC   proliferation and/or redifferentiation of chondrocytes in culture and are
CC   thus useful for treating sports injuries, and arthritis. This is the
CC   amino acid sequence of a novel human PRO protein
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 538;  DB 6;  Length 123;
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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 9
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ID   ABU82583 standard; protein; 123 AA.
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AC   ABU82583;
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DT   26-JUN-2003  (first entry)
XX
DE   Human secreted/transmembrane protein PRO619.
XX
KW   Human; PRO; secreted protein; transmembrane protein;
KW   cardiac insufficiency disorders; angiogenesis; wound healing;
KW   cancerous tumour; immune response; retinal disorder; sight loss;
KW   retinitis pigmentosum; age-related macular degeneration; AMD;
KW   kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;
KW   Crohn's disease; sports injury; arthritis.
XX
OS   Homo sapiens.
XX
PN   US2003032023-A1.
XX
PD   13-FEB-2003.
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PF   14-NOV-2001; 2001US-00990711.
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PR 02-JUL-1998; 98US-0091633P.
PR 02-JUL-1998; 98US-0091646P.
PR 02-JUL-1998; 98US-0091673P.
PR 07-JUL-1998; 98US-0091978P.
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PR 09-JUL-1998; 98US-0092182P.
PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
PR 04-AUG-1998; 98US-0095282P.
PR 04-AUG-1998; 98US-0095285P.
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PR 26-AUG-1998; 98US-0098014P.
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PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
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PR 08-MAR-1999; 99WO-US005028.
PR 12-MAR-1999; 99US-0123957P.
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PR 07-JUL-1999; 99US-0143048P.
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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
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PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
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PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 538; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 10
ABO17816
ID ABO17816 standard; protein; 123 AA.
XX
AC ABO17816;
XX
DT 26-AUG-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO619.
XX
KW Human; secreted and transmembrane protein; PRO; antiinflammatory;
KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;
KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;
KW TNF-alpha release; cell proliferation; cell differentiation;
KW gene expression modulator; proteoglycan release; cytokine release;
KW tumour; inflammatory disease; organ failure; atherosclerosis;
KW cardiac injury; infertility; birth defect; premature aging; AIDS;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;
KW bioreactor; tissue typing.
XX
OS Homo sapiens.
XX
PN US2003032156-A1.
XX
PD 13-FEB-2003.
XX
PF 06-MAY-2002; 2002US-00140474.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
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PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
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PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
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PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
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PR 01-DEC-1999; 99WO-US028634.
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PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
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PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
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PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
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PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
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PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-341980/32.
DR N-PSDB; ACD24053.
XX
PT New secreted and transmembrane PRO nucleic acids, for treating
PT inflammation, organ failure, atherosclerosis, cardiac injury,
PT infertility, birth defects, premature aging, axquired immunodeficiency
PT syndrome (AIDS), or cancer.
XX
PS Claim 12; Fig 402; 660pp; English.
XX

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CC   The invention describes an isolated nucleic acid (I) comprising, or which
CC   has 80 % sequence identity to, or the full-length coding sequence of, one
CC   of 275 nucleotide sequences, and which encodes a corresponding
CC   polypeptide selected from 275 amino acid sequences, where all sequences
CC   are given in the specification. The polypeptide encoded by (I) is used to
CC   detect PRO polypeptides, link a bioactive molecule to a cell expressing a
CC   PRO polypeptide, modulate a biological activity of a cell, stimulate the
CC   release of tumour necrosis factor (TNF)-alpha from human blood, modulate
CC   the uptake of glucose or free fatty acid by cells, stimulate or inhibit
CC   the proliferation or differentiation of cells or gene expression,
CC   stimulate the release of proteoglycans, stimulate the release of cytokine
CC   from peripheral blood mononuclear cells, inhibit the binding of A-peptide
CC   to factor VIIA, or detect the presence of tumour in a mammal. The nucleic
CC   acid and polypeptide encoded by it, are useful for treating inflammatory
CC   diseases, organ failure, atherosclerosis, cardiac injury, infertility,
CC   birth defects, premature aging, acquired immunodeficiency syndrome
CC   (AIDS), cancer, or diabetic complications. The nucleic acid is useful as
CC   hybridisation probes, in chromosome and gene mapping, and in generating
CC   antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,
CC   diagnostics, biosensors or bioreactors. Both are useful in tissue typing.
CC   This is the amino acid sequence of a novel human secreted and
CC   transmembrane PRO polypeptide
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 538;  DB 6;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
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Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
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RESULT 11
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ID   ABU60502 standard; protein; 123 AA.
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AC   ABU60502;
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DT   01-MAY-2003  (first entry)
XX
DE   Human secreted/transmembrane protein, #43.
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KW   Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;
KW   diagnostic; therapeutic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US2002160384-A1.
XX
PD   31-OCT-2002.
XX
PF   14-NOV-2001; 2001US-00992598.
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PR   16-JUN-1997;   97US-0049787P.
PR   17-OCT-1997;   97US-0062250P.
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PR   17-SEP-1998;   98WO-US019437.
PR   07-OCT-1998;   98WO-US021141.
PR   01-DEC-1998;   98WO-US025108.
PR   05-JAN-1999;   99WO-US000106.
PR   08-MAR-1999;   99WO-US005028.
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PR   30-NOV-1999;   99WO-US028313.
PR   01-DEC-1999;   99WO-US028301.
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PR   16-DEC-1999;   99WO-US030095.
PR   20-DEC-1999;   99WO-US030911.
PR   05-JAN-2000; 2000WO-US000219.
PR   06-JAN-2000; 2000WO-US000376.
PR   11-FEB-2000; 2000WO-US003565.
PR   18-FEB-2000; 2000WO-US004341.
PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
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PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-288106/28.
DR N-PSDB; ABX90174.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 12; Fig 68; 650pp; English.
XX
CC The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 12
ABU13884
ID ABU13884 standard; protein; 123 AA.
XX
AC ABU13884;
XX
DT 26-FEB-2003 (first entry)
XX
DE Human PRO619 polypeptide.
XX
KW Human; PRO polypeptide; secreted protein; transmembrane protein;
KW genetic disorder; antibacterial; immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2002103125-A1.
XX
PD 01-AUG-2002.
XX
PF 20-NOV-2001; 2001US-00989731.
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PR 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
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PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
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PR 04-JUN-1998; 98US-0088021P.
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PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.

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PR   22-FEB-2000; 2000WO-US004414.
PR   24-FEB-2000; 2000WO-US004914.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   10-MAR-2000; 2000WO-US006319.
PR   15-MAR-2000; 2000WO-US006884.
PR   20-MAR-2000; 2000WO-US007377.
PR   30-MAR-2000; 2000WO-US008439.
PR   15-MAY-2000; 2000WO-US013358.
PR   17-MAY-2000; 2000WO-US013705.
PR   22-MAY-2000; 2000WO-US014042.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   28-JUL-2000; 2000WO-US020710.
PR   11-AUG-2000; 2000WO-US022031.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   08-NOV-2000; 2000WO-US030952.
PR   01-DEC-2000; 2000WO-US032678.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-JUN-2001; 2001WO-US017800.
PR   20-JUN-2001; 2001WO-US019692.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-JUL-2001; 2001WO-US021735.
PR   28-AUG-2001; 2001US-00941992.
XX
PA   (GETH ) GENENTECH LTD.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein D,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gerber H,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Kljavin IJ,  Napier MA,  Pan J,  Paoni NF;
PI   Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM,  Wood WI;
PI   Zhang Z;
XX
DR   WPI; 2003-102117/09.
DR   N-PSDB; ABX64020.
XX
PT   Novel secreted and transmembrane polypeptide for modulating biological
PT   activity of cell expressing the polypeptide, identifying agonists or
PT   antagonists of polypeptide, and as molecular weight markers.
XX
PS   Claim 12; Fig 68; 649pp; English.
XX
CC   The present invention relates to the isolation of novel human PRO
CC   polypeptides, and the polynucleotide sequences encoding them. The PRO
CC   polypeptides are secreted and transmembrane proteins. The PRO
CC   polypeptides are useful for detecting other PRO polypeptides, for linking
CC   bioactive molecules to cells expressing PRO polypeptides, for modulating
CC   biological activities of cells expressing PRO polypeptides, and for for
CC   identifying agonists or antagonists. The polynucleotide sequences
CC   encoding PRO polypeptides are useful as hybridisation probes, in
CC   chromosome and gene mapping, in the generation of antisense RNA and DNA,
CC   in the preparation of PRO polypeptides, for generating transgenic animals
CC   or knockout animals, to construct hybridisation probes for mapping the
CC   gene which encodes the PRO polypeptide, and for the genetic analysis of
CC   individuals with genetic disorders, in gene therapy, for chromosome
CC   identification, as chromosome markers, and for generating probes for PCR,
CC   Northern analysis, Southern analysis and Western analysis. ABU13860-
CC   ABU14006 represent the human PRO polypeptides of the invention. Note: The
CC   sequence data for this patent was obtained in electronic format directly
CC   from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ   Sequence 123 AA;

  Query Match             100.0%;  Score 538;  DB 6;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
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Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 13
ABU81070
ID   ABU81070 standard; protein; 123 AA.
XX
AC   ABU81070;
XX
DT   23-JUN-2003  (first entry)
XX
DE   Human PRO polypeptide #201.
XX
KW   Human; PRO polypeptide; secreted and transmembrane protein;
KW   anti-PRO antibody; diagnostic assay; gene expression; diabetes;
KW   bone disorder; cartilage disorder; rheumatoid arthritis; obesity;
KW   sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;
KW   hearing loss; coagulation disorder; stroke; heart attack; cardiant;
KW   antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic;
KW   antirheumatic; auditory; cerebroprotective; angiogenic.
XX
OS   Homo sapiens.
XX
PN   US2003004311-A1.
XX
PD   02-JAN-2003.
XX
PF   19-DEC-2001; 2001US-00028072.
XX
PR   18-JUN-1997;   97US-0049911P.
PR   26-AUG-1997;   97US-0056974P.
PR   17-SEP-1997;   97US-0059113P.
PR   17-SEP-1997;   97US-0059115P.
PR   17-SEP-1997;   97US-0059117P.
PR   17-SEP-1997;   97US-0059122P.
PR   17-SEP-1997;   97US-0059184P.
PR   18-SEP-1997;   97US-0059263P.
PR   19-SEP-1997;   97US-0059352P.
PR   19-SEP-1997;   97US-0059588P.
PR   24-SEP-1997;   97US-0059836P.
PR   17-OCT-1997;   97US-0062250P.
PR   17-OCT-1997;   97US-0062285P.
PR   17-OCT-1997;   97US-0062287P.
PR   17-OCT-1997;   97US-0063755P.
PR   24-OCT-1997;   97US-0062814P.
PR   24-OCT-1997;   97US-0062816P.
PR   24-OCT-1997;   97US-0063045P.
PR   24-OCT-1997;   97US-0063082P.
PR   24-OCT-1997;   97US-0063127P.
PR   27-OCT-1997;   97US-0063327P.
PR   27-OCT-1997;   97US-0063329P.
PR   28-OCT-1997;   97US-0063550P.
PR   28-OCT-1997;   97US-0063561P.
PR   29-OCT-1997;   97US-0063704P.
PR   29-OCT-1997;   97US-0063733P.
PR   29-OCT-1997;   97US-0063735P.
PR   29-OCT-1997;   97US-0063738P.
PR   03-NOV-1997;   97US-0064248P.
PR   07-NOV-1997;   97US-0064809P.
PR   12-NOV-1997;   97US-0065186P.
PR   17-NOV-1997;   97US-0065846P.
PR   21-NOV-1997;   97US-0066364P.
PR   24-NOV-1997;   97US-0066453P.
PR   24-NOV-1997;   97US-0066511P.
PR   24-NOV-1997;   97US-0066770P.
PR   11-DEC-1997;   97US-0069212P.
PR   11-DEC-1997;   97US-0069278P.
PR   11-DEC-1997;   97US-0069334P.
PR   16-DEC-1997;   97US-0069694P.
PR   23-JAN-1998;   98US-0072320P.
PR   04-FEB-1998;   98US-0073612P.
PR   09-FEB-1998;   98US-0074086P.
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PR 09-FEB-1998; 98US-0074092P.
PR 12-MAR-1998; 98US-0077791P.
PR 20-MAR-1998; 98US-0078910P.
PR 25-MAR-1998; 98US-0079294P.
PR 27-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079728P.
PR 31-MAR-1998; 98US-0080165P.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-352836/33.
DR N-PSDB; ACA67194.
XX
PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid
PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
PT heart attack.
XX
PS Claim 12; Fig 402; 643pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the treatment of diabetes, bone and/or cartilage disorders
CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,
CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders
CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells, tissues or
CC serum, and for affinity purification of PRO from recombinant cell culture
CC or natural sources. ABU80870-ABU81144 represent the human PRO
CC polypeptides of the invention. Note: The sequence data for this patent
CC was obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
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Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 14
ABU72469
ID ABU72469 standard; protein; 123 AA.
XX
AC ABU72469;
XX
DT 17-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO619.
XX
KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;
KW PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy;
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;
KW drug screening.
XX
OS Homo sapiens.
XX
PN US2003003531-A1.
XX
PD 02-JAN-2003.
XX
PF 19-NOV-2001; 2001US-00989734.
XX
PR 16-JUN-1997; 97US-0049787P.
PR 17-OCT-1997; 97US-0062250P.
PR 05-NOV-1997; 97WO-US020069.
PR 12-NOV-1997; 97US-0065186P.
PR 13-NOV-1997; 97US-0065311P.
PR 24-NOV-1997; 97US-0066770P.
PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
PR 28-APR-1998; 98US-0083322P.
PR 07-MAY-1998; 98US-0084600P.
PR 28-MAY-1998; 98US-0087106P.
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088025P.
PR 04-JUN-1998; 98US-0088026P.

PR 04-JUN-1998; 98US-0088028P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2003-352829/33.
DR N-PSDB; ACA64242.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 12; Fig 68; 663pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 123 AA;

Query Match 100.0%; Score 538; DB 6; Length 123;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 15
ABU66770
ID ABU66770 standard; protein; 123 AA.
XX
AC ABU66770;
XX
DT 23-MAY-2003 (first entry)
XX
DE Human PRO polypeptide #201.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036180-A1.
XX

PD 20-FEB-2003.
XX
PF 09-MAY-2002; 2002US-00143114.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
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PR 01-MAR-2001; 2001WO-US006666.
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PR 14-MAR-2001; 2001US-00808689.
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PR 01-JUN-2001; 2001US-00872035.
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PR 05-JUN-2001; 2001US-00874503.
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PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-332040/31.
DR N-PSDB; ACA03803.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 402; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 123 AA;

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	538	100.0	123	9	US-09-989-723-117	Sequence 117, App
3	538	100.0	123	9	US-09-989-279-117	Sequence 117, App
4	538	100.0	123	9	US-09-989-727-117	Sequence 117, App
5	538	100.0	123	9	US-09-989-731-117	Sequence 117, App
6	538	100.0	123	9	US-09-989-732-117	Sequence 117, App
7	538	100.0	123	9	US-09-991-073-117	Sequence 117, App
8	538	100.0	123	9	US-09-990-442-117	Sequence 117, App
9	538	100.0	123	9	US-09-991-163-117	Sequence 117, App
10	538	100.0	123	9	US-09-993-604-117	Sequence 117, App
11	538	100.0	123	9	US-09-990-456-117	Sequence 117, App
12	538	100.0	123	9	US-09-989-721-117	Sequence 117, App
13	538	100.0	123	9	US-09-992-598-117	Sequence 117, App
14	538	100.0	123	9	US-09-981-876-200	Sequence 200, App
15	538	100.0	123	9	US-09-989-293A-117	Sequence 117, App
16	538	100.0	123	9	US-09-989-735-117	Sequence 117, App
17	538	100.0	123	9	US-09-990-444-117	Sequence 117, App
18	538	100.0	123	9	US-09-991-181-117	Sequence 117, App
19	538	100.0	123	9	US-09-989-730-117	Sequence 117, App
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21	538	100.0	123	9	US-09-993-687-117	Sequence 117, App
22	538	100.0	123	10	US-09-989-734-117	Sequence 117, App
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25	538	100.0	123	10	US-09-148-545-200	Sequence 200, App
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32	538	100.0	123	10	US-09-998-156-117	Sequence 117, App
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35	538	100.0	123	10	US-09-997-514-117	Sequence 117, App
36	538	100.0	123	10	US-09-997-573-117	Sequence 117, App
37	538	100.0	123	10	US-09-991-172-117	Sequence 117, App
38	538	100.0	123	10	US-09-990-726-117	Sequence 117, App
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45	538	100.0	123	10	US-09-989-729A-117	Sequence 117, App

ALIGNMENTS

RESULT 1
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; Sequence 117, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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Query Match 100.0%; Score 538; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-989-279-117
; Sequence 117, Application US/09989279
; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
; APPLICANT: Gerber,Hanspeter
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
; APPLICANT: Gurney,Austin L.
; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-07-09

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; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 5
US-09-989-731-117
; Sequence 117, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Fong,Sherman
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; APPLICANT: Gerritsen,Mary E.
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; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,J.Christopher
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; APPLICANT: Kljavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C70
; CURRENT APPLICATION NUMBER: US/09/989,731
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
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Query Match 100.0%; Score 538; DB 9; Length 123;
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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; Sequence 117, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123
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RESULT 7
US-09-991-073-117
; Sequence 117, Application US/09991073
; Patent No. US20020127576A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
; APPLICANT: Desnoyers,Luc
; APPLICANT: Eaton,Dan L.
; APPLICANT: Ferrara,Napoleone
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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

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  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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; Sequence 117, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
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;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C8
;  CURRENT APPLICATION NUMBER: US/09/990,442
;  CURRENT FILING DATE:  2001-11-14
;  PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 538; DB 9; Length 123;
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Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi,Avi J.
; APPLICANT: Baker,Kevin P.
; APPLICANT: Botstein,David
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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Query Match 100.0%; Score 538; DB 9; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.9e-50;
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Qy 1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60

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RESULT 10
US-09-993-604-117
; Sequence 117, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
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;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
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;  APPLICANT:  Watanabe, Colin K.
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;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
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;  CURRENT FILING DATE:  2001-11-14
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; APPLICANT: Botstein,David
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; APPLICANT: Zhang, Zemin
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;  PRIOR APPLICATION NUMBER: 60/092182
;  PRIOR FILING DATE: 1998-07-09

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; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,J.Christopher
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
;  APPLICANT:  Pan,James
;  APPLICANT:  Paoni,Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2730P1C20
;  CURRENT APPLICATION NUMBER: US/09/992,598
;  CURRENT FILING DATE:  2001-11-14
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RESULT 14
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; Sequence 200, Application US/09981876
; Patent No. US20020164669A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
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;  NUMBER OF SEQ ID NOS: 280
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Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 15
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; Sequence 117, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi,Avi J.
;  APPLICANT:  Baker,Kevin P.
;  APPLICANT:  Botstein,David
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Eaton,Dan L.
;  APPLICANT:  Ferrara,Napoleone
;  APPLICANT:  Fong,Sherman
;  APPLICANT:  Gerber,Hanspeter
;  APPLICANT:  Gerritsen,Mary E.
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;  APPLICANT:  Kljavin,Ivar J.
;  APPLICANT:  Napier,Mary A.
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;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Watanabe, Colin K.
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  APPLICANT:  Zhang, Zemin
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;  TITLE OF INVENTION:  Acids Encoding the Same
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GenCore version 5.1.6

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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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ALIGNMENTS

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; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
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; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT:  Jobert, S.
;  APPLICANT:  Giordano, J.Y.
;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE:  2000-07-21
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;   FEATURE:
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;   LOCATION: -20..-1
US-09-621-976-5367

  Query Match             100.0%;  Score 538;  DB 4;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-52;
  Matches   99;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 LDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIP 84

Qy         61 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              |||||||||||||||||||||||||||||||||||||||
Db         85 DRFSAAKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 123


RESULT 3
US-07-988-925-16
; Sequence 16, Application US/07988925
; Patent No. 5585097
;  GENERAL INFORMATION:
;    APPLICANT:  Bolt, Sarah L
;    APPLICANT:  Clark, Michael R
;    APPLICANT:  Gorman, Scott D
;    APPLICANT:  Routledge, Edward G
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  antibody preparation
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye pc
;      STREET:  11th Floor, 1100 No. 5585097th Glebe Road
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,925
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206422.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/GB92/01933
;      FILING DATE:  21-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mitchard, Leonard C
;      REGISTRATION NUMBER:  29009
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164000
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-988-925-16

  Query Match              35.1%;  Score 189;  DB 1;  Length 110;
  Best Local Similarity    46.4%;  Pred. No. 1.1e-13;
  Matches   39;  Conservative   14;  Mismatches   25;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:  .:|||||  :  | :  | ||||| | ||  :::    :|  ||  :|||||  :
Db         14 PGKTVIISCTLSSGN--IENNYVHWYQQRPGRAPTTVIF----DDDKRPDGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :| ||:|||||
Db         68 DRSSNSASLTISGLQTEDEADYYC 91


RESULT 4
US-08-362-780-16
; Sequence 16, Application US/08362780
; Patent No. 5968509
;  GENERAL INFORMATION:
;    APPLICANT:  Gorman, Scott D
;    APPLICANT:  Routledge, Edward G
;    APPLICANT:  Waldmann, Herman
;    TITLE OF INVENTION:  Antibody Preparation
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon and Vanderhye pc
;      STREET:  8th Floor, 1100 No. 5968509th Glebe Road
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/362,780
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/862,543
```

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;       FILING DATE:  23-JUNE-1992
;       APPLICATION NUMBER:  GB 9021679.7
;       FILING DATE:  05-OCT-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/GB91/01726
;       FILING DATE:  04-OCT-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Mitchard, Leonard C
;       REGISTRATION NUMBER:  29009
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164000
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  110 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-362-780-16

  Query Match             35.1%;  Score 189;  DB 2;  Length 110;
  Best Local Similarity   46.4%;  Pred. No. 1.1e-13;
  Matches   39;  Conservative   14;  Mismatches   25;  Indels    6;  Gaps    2;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              ||:   :|||||  :  | :  | ||||| | ||  :::    :|  ||  :|||||  :
Db         14 PGKTVIISCTLSSGN--IENNYVHWYQQRPGRAPTTVIF----DDDKRPDGVPDRFSGSI 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
              | : |:  |||| :| ||:|||||
Db         68 DRSSNSASLTISGLQTEDEADYYC 91


RESULT 5
US-08-918-148-74
; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
;  APPLICANT: Adams, Camellia
;  APPLICANT: W.
;  APPLICANT: Carter, Paul J.
;  APPLICANT: Fendly, Brian M.
;  APPLICANT: Gurney, Austin L.
;  TITLE OF INVENTION: Agonist Antibodies
;  FILE REFERENCE: P0979
;  CURRENT APPLICATION NUMBER: US/08/918,148A
;  CURRENT FILING DATE: 1997-08-25
;  NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: artificial
US-08-918-148-74

  Query Match             35.0%;  Score 188.5;  DB 4;  Length 249;
  Best Local Similarity   49.4%;  Pred. No. 3.3e-13;
  Matches   42;  Conservative   13;  Mismatches   23;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   :| ||||||  | ||: |:|  |    :||: :||||||:|
Db        150 PGQSITISCTGTSSGVGGYNY-VSWYQQHPGKAPKLLIYGNS----NRPSGVPDRFSASK 204

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   |||| :| ||:|||:||
Db        205 --SGNTASLTISGLQAEDEADYFCS 227


RESULT 6
US-09-157-370-5
; Sequence 5, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
;  APPLICANT: STEIPE, Boris
;  APPLICANT: STEINBACHER, Stefan
;  TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
;  FILE REFERENCE: P8341-8072
;  CURRENT APPLICATION NUMBER: US/09/157,370A
;  CURRENT FILING DATE: 1998-09-21
;  EARLIER APPLICATION NUMBER: 08/765,179
;  EARLIER FILING DATE: 1997-01-14
;  EARLIER APPLICATION NUMBER: PCT/EP95/02626
;  EARLIER FILING DATE: 1995-07-06
;  EARLIER APPLICATION NUMBER: DE/P44 25 115.7
;  EARLIER FILING DATE: 1994-07-15
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-157-370-5

  Query Match             34.2%;  Score 184;  DB 3;  Length 109;
  Best Local Similarity   43.3%;  Pred. No. 3.8e-13;
  Matches   42;  Conservative   15;  Mismatches   24;  Indels   16;  Gaps    4;

Qy          6 VFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
              | |||   :||:     :      ||||||: | ||: ::|    :|: ||: ||||||
Db         12 VSPGQTVTISCSGDSLGIGY----VSWYQQKPGQAPKLVIY----DDNKRPSGIPDRFSG 63

Qy         66 AKDEAHNACVLTISPVQPEDDADYYC------SVGYG 96
              :|  : |   |||| :| ||:|||||      || :|
Db         64 SK--SGNTASLTISGLQAEDEADYYCQSWDSSSVVFG 98


RESULT 7
US-10-039-785-42
; Sequence 42, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF550
;  CURRENT APPLICATION NUMBER: US/10/039,785
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: 60/369,860
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/341,237
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/331,310
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: 60/331,044
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 60/327,364
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/323,807
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: 60/309,176
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/294,981
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/293,473
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: T1014A04 scFv
US-10-039-785-42

  Query Match             33.9%;  Score 182.5;  DB 4;  Length 245;
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  Best Local Similarity   45.9%;  Pred. No. 1.5e-12;
  Matches   39;  Conservative   15;  Mismatches   24;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   :| ||||||  | ||: ::|  ::    ||: :||||| :|
Db        148 PGQSVTISCTGTTSDVGGYNY-VSWYQQHPGKAPKLMIYGVNQ----RPSGVPDRFSGSK 202

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |  ||:| :| ||:||||||
Db        203 --SGNTASLTVSGLQAEDEADYYCS 225


RESULT 8
US-09-240-274-63
; Sequence 63, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain O01
US-09-240-274-63

  Query Match             33.7%;  Score 181.5;  DB 3;  Length 110;
  Best Local Similarity   44.0%;  Pred. No. 7.4e-13;
  Matches   37;  Conservative   17;  Mismatches   23;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| |  ::    ||| |||| |:||: ::|     |::||: :||||| :|
Db         13 PGQRVTISCTGSSSNIG-APYGVHWYQQFPGTAPKLVIY----NDNNRPSGVPDRFSGSK 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
                :  :  | |: :| ||:|||||
Db         68 --SGTSASLAITGLQAEDEADYYC 89


RESULT 9
US-09-025-769B-34
; Sequence 34, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)596-9000
;      TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-34

  Query Match             33.6%;  Score 181;  DB 4;  Length 107;
  Best Local Similarity   42.6%;  Pred. No. 8.1e-13;
  Matches   40;  Conservative   13;  Mismatches   31;  Indels   10;  Gaps    3;

Qy          6 VFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
              | ||| |::||:       : |   |||||: | ||  ::|    :|  ||: ||:|||
Db         12 VAPGQTARISCSGD----ALGDKYASWYQQKPGQAPVLVIY----DDSDRPSGIPERFSG 63

Qy         66 AKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
                 :  : |   ||||  | ||:|||||   |  |
Db         64 S--NSGNTATLTISGTQAEDEADYYCQQHYTTPP 95


RESULT 10
US-09-025-769B-55
; Sequence 55, Application US/09025769B
; Patent No. 6300064
;  GENERAL INFORMATION:
;    APPLICANT:  Knappik, Achim
;    APPLICANT:  Pack, Peter
;    APPLICANT:  Ilag, Vic
;    APPLICANT:  Ge, Liming
;    APPLICANT:  Moroney, Simon
;    APPLICANT:  Plueckthun, Andreas
;    TITLE OF INVENTION:  Protein/(Poly)peptide libraries
;    NUMBER OF SEQUENCES:  373
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET:  1251 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10021
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/025,769B
;      FILING DATE:  18-FEB-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 95 11 3021.0
;      FILING DATE:  18-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER:  27,794
;      REFERENCE/DOCKET NUMBER:  MORPHO/5
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  (212)596-9000
;       TELEFAX:  (212)596-9090
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  107 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-025-769B-55

  Query Match             33.6%;  Score 181;  DB 4;  Length 107;
  Best Local Similarity   42.6%;  Pred. No. 8.1e-13;
  Matches   40;  Conservative   13;  Mismatches   31;  Indels   10;  Gaps    3;

Qy          6 VFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSA 65
              | ||| |::||:       : |   |||||: | ||  ::|    :|  ||: ||:|||
Db         12 VAPGQTARISCSGD----ALGDKYASWYQQKPGQAPVLVIY----DDSDRPSGIPERFSG 63

Qy         66 AKDEAHNACVLTISPVQPEDDADYYCSVGYGFSP 99
              :   : |   ||||  | ||:|||||   |   |
Db         64 S--NSGNTATLTISGTQAEDEADYYCQQHYTTPP 95


RESULT 11
US-10-039-785-48
; Sequence 48, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF550
;  CURRENT APPLICATION NUMBER: US/10/039,785
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: 60/369,860
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/341,237
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/331,310
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: 60/331,044
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 60/327,364
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/323,807
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: 60/309,176
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/294,981
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/293,473
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: T1014F11 scFv
US-10-039-785-48

  Query Match             33.4%;  Score 179.5;  DB 4;  Length 245;
  Best Local Similarity   45.9%;  Pred. No. 3.2e-12;
  Matches   39;  Conservative   13;  Mismatches   26;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   | ||||||  | ||: ::|    |   ||: :|||||  :|
Db        148 PGQSVTISCTGTSSDVGGYKY-VSWYQQHPGKAPKLMIY----EVSMRPSGVPDRFSGSK 202

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   ||:| :| ||:|||||:
Db        203 --SGNTASLTVSGLQAEDEADYYCA 225


RESULT 12
US-10-039-785-49
; Sequence 49, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
;  APPLICANT: Salcedo et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: PF550
;  CURRENT APPLICATION NUMBER: US/10/039,785
;  CURRENT FILING DATE:  2002-05-07
;  PRIOR APPLICATION NUMBER: 60/369,860
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: 60/341,237
;  PRIOR FILING DATE: 2001-12-20
;  PRIOR APPLICATION NUMBER: 60/331,310
;  PRIOR FILING DATE: 2001-11-14
;  PRIOR APPLICATION NUMBER: 60/331,044
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 60/327,364
;  PRIOR FILING DATE: 2001-10-09
;  PRIOR APPLICATION NUMBER: 60/323,807
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: 60/309,176
;  PRIOR FILING DATE: 2001-08-02
;  PRIOR APPLICATION NUMBER: 60/294,981
;  PRIOR FILING DATE: 2001-06-04
;  PRIOR APPLICATION NUMBER: 60/293,473
;  PRIOR FILING DATE: 2001-05-25
;  NUMBER OF SEQ ID NOS: 66
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: T1014G04 scFv
US-10-039-785-49

  Query Match             33.2%;  Score 178.5;  DB 4;  Length 245;
  Best Local Similarity   44.7%;  Pred. No. 4.1e-12;
  Matches   38;  Conservative   15;  Mismatches   25;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |   :| ||||||  | ||| ::     | : ||: :|:||| :|
Db        148 PGQSVTISCTGTSSDVGSYEY-VSWYQQHPGKAPRLMI----SEVNKRPSGVPNRFSGSK 202

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   ||:| :| :|:||||||
Db        203 --SGNTASLTVSGLQADDEADYYCS 225


RESULT 13
US-09-240-274-68
; Sequence 68, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
;   LENGTH: 108
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain R01
US-09-240-274-68

  Query Match             32.8%;  Score 176.5;  DB 3;  Length 108;
  Best Local Similarity   45.9%;  Pred. No. 2.6e-12;
  Matches   39;  Conservative   12;  Mismatches   27;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |    : ||||||  | ||: |    : |   ||: :||||| :|
Db         13 PGQSVTISCTGASSDVGAYKH-VSWYQQHPGKAPKLL----THEGTKRPSGVPDRFSGSK 67

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   ||:| :| ||:||||||
Db         68 --SGNTASLTVSGLQAEDEADYYCS 90


RESULT 14
US-08-958-201-14
; Sequence 14, Application US/08958201
; Patent No. 5977319
;  GENERAL INFORMATION:
;    APPLICANT:  Pope, Anthony R
;    APPLICANT:  Pritchard, Kevin
;    APPLICANT:  Williams, Andrew J
;    APPLICANT:  Johnson, Kevin S
;    TITLE OF INVENTION:  Specific binding members for estradiol;
;    TITLE OF INVENTION:  materials and methods
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall O'Toole Gerstein Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/958,201
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/028,897
;      FILING DATE:  21-OCT-1996
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  1C/2D
US-08-958-201-14

  Query Match             32.8%;  Score 176.5;  DB 2;  Length 111;
  Best Local Similarity   45.9%;  Pred. No. 2.7e-12;
  Matches   39;  Conservative   14;  Mismatches   25;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| :   |    | ||||||  | ||: :::    |  :||: :|:||| :|
Db         14 PGQSITISCTGTSSDVGGYKY-VSWYQQHPGKAPKLMIF----EVSNRPSGVPNRFSGSK 68

Qy         68 DEAHNACVLTISPVQPEDDADYYCS 92
                : |   |||| :| ||:||||||
Db         69 --SGNTASLTISGLQAEDEADYYCS 91


RESULT 15
US-09-240-274-64
; Sequence 64, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain O02
US-09-240-274-64

  Query Match             32.8%;  Score 176.5;  DB 3;  Length 112;
  Best Local Similarity   42.9%;  Pred. No. 2.7e-12;
  Matches   36;  Conservative   16;  Mismatches   25;  Indels    7;  Gaps    3;

Qy          8 PGQVAQLSCTLSPQHVTIRDYGVSWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAK 67
              |||   :||| |   :  | | | |||   |:||: |:|     :|:||: :||||| :|
Db         13 PGQTVTISCTGSSSSIGAR-YDVHWYQHLPGTAPKLLIY----GNHNRPSGVPDRFSGSK 67

Qy         68 DEAHNACVLTISPVQPEDDADYYC 91
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Db         68 --SGTSASLAITGLQAEDEAEYYC 89


Search completed: June 28, 2004, 08:28:44
Job time : 15.7162 secs
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